

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 11, 2005, 06:54:09 ; Search time 112 Seconds
(without alignments)
5654.579 Million cell updates/sec

Title: US-09-994-365-1

Perfect score: 891
Sequence: 1 cccctcggggtccacagca.....taaaacatgtttctta 891

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfill1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	160	18.0	248	US-09-621-976-9776	Sequence 9776, Ap
2	80.8	9.1	7218	US-08-232-463-14	Sequence 14, Appl
3	45.4	5.1	2220	US-08-765-907A-14	Sequence 14, Appl
4	45.4	5.1	4496	US-08-765-907A-6	Sequence 6, Appl
5	44.8	5.0	53526	US-08-658-136-2	Sequence 2, Appl
6	44.8	5.0	53577	US-08-658-136-1	Sequence 1, Appl
7	43.8	4.9	645	US-08-403-852D-9	Sequence 9, Appl
8	43.8	4.9	645	US-08-510-646B-9	Sequence 9, Appl
9	43.8	4.9	645	US-09-231-818-9	Sequence 9, Appl
10	43.8	4.9	645	US-09-635-359B-9	Sequence 9, Appl
11	42.6	4.8	1926	US-09-249-585A-2	Sequence 2, Appl
12	42.6	4.8	1926	US-09-410-389-3	Sequence 3, Appl
13	42.6	4.8	2580	US-09-050-863-2	Sequence 2, Appl
14	42.6	4.8	2580	US-09-359-081-2	Sequence 2, Appl
15	42.6	4.8	5452	US-09-130-114-1	Sequence 1, Appl
16	42.6	4.8	8705	US-09-647-344A-14	Sequence 14, Appl
17	42.6	4.8	9600	US-08-910-647-1	Sequence 1, Appl
18	42.6	4.8	9600	US-09-620-925-1	Sequence 1, Appl
19	42.6	4.8	10596	US-07-884-811-15	Sequence 15, Appl
20	42.6	4.8	10596	US-07-885-971-15	Sequence 15, Appl
21	42.6	4.8	10596	US-08-087-783A-15	Sequence 15, Appl
22	42.6	4.8	10596	US-08-194-088B-15	Sequence 15, Appl
23	42.6	4.8	10596	US-08-194-087-15	Sequence 15, Appl
24	42.6	4.8	10596	BCT-US93-04648-15	Sequence 15, Appl
25	42.6	4.8	16080	US-09-724-566A-48	Sequence 48, Appl
26	42.6	4.8	15231	US-09-128-155-16	Sequence 16, Appl
27	41	4.6	364	US-09-621-976-17202	Sequence 17202, A

28	41	4.6	1166	US-09-072-596-323	Sequence 323, App
29	41	4.6	1166	US-09-072-967-328	Sequence 328, App
30	41	4.6	3297	US-09-620-312D-417	Sequence 417, App
31	39.2	4.4	44377	US-08-804-227C-7	Sequence 7, Appl
32	39.2	4.4	44377	US-08-804-198-1	Sequence 1, Appl
33	38.4	4.3	354	US-09-621-976-13855	Sequence 13855, A
34	38.2	4.3	320	US-09-165-264-7	Sequence 7, Appl
35	37.8	4.2	289	US-09-007-005-17	Sequence 17, Appl
36	37.8	4.2	289	US-09-244-796-17	Sequence 17, Appl
37	37.8	4.2	1660	US-09-637-367-21	Sequence 21, Appl
38	37.8	4.2	1660	US-09-918-909A-21	Sequence 21, Appl
39	37.8	4.2	1738	US-09-918-909A-27	Sequence 27, Appl
40	37.6	4.2	1926	US-09-249-585A-4	Sequence 4, Appl
41	37.6	4.2	1931	US-09-130-114-2	Sequence 2, Appl
42	37.4	4.2	6649	US-09-789-451-384	Sequence 384, App
43	37.2	4.2	711	US-09-252-991A-15345	Sequence 15345, A
44	37.2	4.2	831	US-09-252-991A-15299	Sequence 15299, A
45	37.2	4.2	861	US-09-252-991A-15491	Sequence 15491, A

ALIGNMENTS

```
RESULT 1
US-09-621-976-9776/c
: Sequence 9776, Application US/096221976
: Patent No. 6639063
: GENERAL INFORMATION:
: APPLICANT: Dumas Milne Edwards, J.B.
: APPLICANT: Giordano, J.Y.
: TITLE OF INVENTION: ESTs and Encoded Human Proteins.
: FILE REFERENCE: GENSET 054PR2
: CURRENT APPLICATION NUMBER: US/09/621.976
: NUMBER OF SEQ ID NOS: 19335
: SOFTWARE: Patent.pm
: SEQ ID NO 9776
: LENGTH: 248
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 188
: OTHER INFORMATION: n=a, g, c or t
US-09-621-976-9776

Query Match      18.0%; Score 160; DB 4; Length 248;
Best Local Similarity 93.0%; Pred. No. 8.6e-36;
Matches 173; Conservative 5; Mismatches 5; Indels 3; Gaps 1;

QY 293 CTGAAGTCGAGTGTGCCCCCTGAGACCGCTTGAAGGATCCTCTTCAACTCCCGGC 352
DB 186 CTGAAGTCGAGTGTGCCCCCTGAGACCGCTTGAAGGATCCTCTTCAACTCCCGGC 127
QY 353 CTGACGACCTTGCGCGGAGGAGCCCGCC---AGCCCCGAGAAACCCCTGAGCTCTGCGCC 409
DB 126 CTGACGACCTTGCGCGGAGGAGCCCGCCCGCCCGGAGAAACCCCTGAGCTCTGCGCC 67
QY 410 CTGAGTGTGCAACCGACCTTCAAGAGGAGCCAGACTTGAACCCACCCCGGAGAGTACA 469
DB 66 CTGAGTGTGCAACCGACCTTCAAGAGGAGCCAGACTTGAACCCACCCCGGAGAGTACA 7
QY 470 GATTAAT 475
DB 6 GATTAAT 1

RESULT 2
US-08-232-463-14
: Sequence 14, Application US/08232463
: Patent No. 5670367
: GENERAL INFORMATION:
```

APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-F15
US-08-232-463-14

Query Match 9.1%; Score 80.8; DB 1; Length 7218;
Best Local Similarity 4.9%; Pred. No. 9.8e-13;
Matches 19; Conservative 237; Mismatches 134; Indels 0; Gaps 0

OY	480	TCCCTCAGCGCTTGTGTTCCACGCATTCAGGACCACGCCCTCTCACCTCTGA	539
Dd	1090	YYY	1149
OY	540	TTCCCGTGAAATTCTCCCAATTTAGCCMATGCTCTTAACCTCTTCTCATTCCTCGG	599
Dd	1150	YYY	1209
OY	600	TTTTATTCTGAACCCGTAGGTGGTGTCTCAATAATTCTGTCCTCCCTCGAATCAT	659
Dd	1210	YYY	1269
OY	660	ACTTAGTCTCATACGCCCCGTTTTTTCCTCTGACAGCTTAAGCTACTCTCACTCG	719
Dd	1270	YYY	1329
OY	720	CCTCCAGGCGTCGGGCCCACTACTCTCCACCGCGTCTTCTGCCC GGCGATCGTGG	779
Dd	1330	YYY	1389
OY	780	GCAAGGCTATGTA CTGTGTTCCCTTCGACCACTGGAGCGCGGAGGAATATAC	839
Dd	1390	YYGTACAAATCTTCT	1449
OY	840	TAGACAGCTGCTGCTTCCATGAAGAAGAA	869

Db 1450 ATCTCTTAAGTCTGATAGTAA 1479

```

RESULT 3
US-08-765-907A-14
; Sequence 14, Application US/08765907A
; Patent No. 6352839
; GENERAL INFORMATION:
; APPLICANT: BLANC, Veronique
; APPLICANT: THIBAUT, Denis
; APPLICANT: BARRAS-JACOUES, Nathalie
; APPLICANT: BLANCHE, Francis
; APPLICANT: COUZET, Joel
; APPLICANT: BARRIERE, Jean-Claude
; APPLICANT: DEBUSSCHE, Laurent
; APPLICANT: FAMECHON, Alain
; APPLICANT: PARIS, Jean-Marc
; APPLICANT: DUTRUC-ROSSET, Gilles
; TITLE OF INVENTION: Streptogramins And Method For Preparing Same By
; TITLE OF INVENTION: Mutasynthesis
; FILE REFERENCE: Streptogramin genes
; CURRENT APPLICATION NUMBER: US/08/765, 907A
; CURRENT FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: Streptomyces pristinaespiralis
US-08-765-907A-14

```

Query Match	5.1%;	Score 45.4;	DB 3;	Length 220;
Best Local Similarity	46.0%;	Pred. No. 0.006;		
Matches 192;	Conservative	0;	Mismatches 221;	Indels 4;
				Gaps 1

QY 1. CAGAGGACCCGAGCTGAGGCCAACCAGGCTTTGGGGGCGAGTACATGACATGATCTCA 73
|||
Db 248 CCACCGACGACCCGAGCTGGGCTTGAAGCCGGGGTATCACCGAATGGAGACTGGCGCTGC 307
QY 74 ACTGGAAAGCTCTGGGGATCTGGTCTTTGGCTCTGACACGAGAGGCAATTCAGGACGG 133
|||
Db 308 TCGGGGGTGTGCTGGGGCGACAGAGGCTGTGGCTGTGGCCGGGCGCCCGCTGTCCACG 367
QY 134 AGGGCCACCCCTCTTCACCCAACCGGAGAGACCGAGAGAGGACAGCTCCCAATTGC 192
|||
Db 368 CACCCGAACCTTTCAACGGCGCC---ACAGCGCATTCGCGCAGACGGGCAAGGGCTG 422
QY 194 CTGAGGGGCCCCCAGTCCCCCGGTGAACCTGTGGGCCAGGGGCAACCCCTCTTTTGAATC 253
|||
Db 424 TTGGCAATATCCTCTCCCGCTGACCGGTGCGCTACACTGGCTGACCGTCCGCA 483
QY 254 CTCGCGCTTACCGGCCCAATGCTCTCCCTGAGAGACTTGCCTGAATACTGAGTGTGGCCC 313
|||
Db 484 CTGCCCGCGAGCTGTGGCGCGCAACGCGCCACAACCGCGACGGGCACTGTATGGCCGTGCC 543
QY 314 CTGAACCGGCTTGAAGACGATCTCTTCAACTCCCCGCGCTGACGACCTTTGGCGGAG 373
|||
Db 544 CACCGGCACTTGCCTCCGCTTGGCGCTGCACTTCAACCCGAAATGATCAGCAGGAAAC 603
QY 374 GACCCGAGCCCCGAGAAACCCGTGGGCTCTGGCCCGAGGTGAGCAACCGACCTC 430
|||
Db 604 GGGCAACGGATGCTGCCAATTTCCGCGAATCTGTCTCTGGCGCGCGGCGACCTCG 660

RESULT 4
US-08-765-907A-6
; Sequence 6, Application US/08765907N
; Patent No. 6352839
; GENERAL INFORMATION:
; APPLICANT: BLANC, Veronique
; APPLICANT: THIBAUT, Denis
; APPLICANT: BAWMS-JACQUES, Nathalie

APPLICANT: BLANCHE, Francis
APPLICANT: COUZET, Joel
APPLICANT: BARRIERE, Jean-Claude
APPLICANT: DEBUSCHE, Laurent
APPLICANT: FAMECHON, Alain
APPLICANT: PARIS, Jean-Marc
APPLICANT: DITRUC-ROSETT, Gilles
TITLE OF INVENTION: Streptogramins And Method For Preparing Same By
TITLE OF INVENTION: Mutasyntaseis
FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/08/765,907A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 4496
TYPE: DNA
ORGANISM: Streptomyces pristinaespiralis
US-08-765-907A-6

Query Match 5.1%; Score 45.4; DB 3; Length 4496;
Best Local Similarity 46.0%; Pred. No. 0.0082;
Matches 192; Conservative 0; Mismatches 221; Indels 4; Gaps 1;

14 CCAGGACACCCAGCTCAGCCACCCAGCTTTGGGGGCGAGTACATAGCATGATCTCA 73
3205 CCACGACACGACGACCTGGGCTCAGCCGCGGATGATCAGGATGGACCTGCCGCTGC 3264
74 ACTGGAAGCTCTGGGGATCTTGCTTTGCTGCAACGAGGAGGATCTCAGGACGCG 133
3265 TCGGGGGTGTCTGGGCGACACGAGGCGCTGTGCTGCGCGGCGCGCTGCTCAGC 3324
134 AGGGGACCCCTCTCAGCCACCGGAGAGACGAGAGGAGGAGGCTCCCAACATTC 193
3325 CACCGGACCTTTGACGCGCGC---ACAGGACATCGGACGAGGAGGAGGCGCTG 3380
194 CTGAGGAGCCCGGAGTCTCCGAGTACCTTTGGCCAGGAGGACCCCTCTTTGAAATC 253
3381 TTGGCGAAGATCCCTCTCCGCTGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 3440
254 CTGCGCTACCCGCGGCGGAGTGTCTGAGAGAGACCTGGAATGAGTCTGCGCC 313
3441 CTGCGCGCGGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3500
314 CTGAACCGGCTTGAAGGAGTCTCTCACTCCCGGCGGCTGAGAGACCTTTGGCGGAG 373
3501 CACCGGACCTGCGCGGCTTGGGCTGAGTTCACCCGAGATGAGAGGAGGAGGAG 3560
374 GACCGGACCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 430
3561 GGCACCGGAGTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3617

RESULT 5
US-08-658-136-2
Sequence 2, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA

ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17,8
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 53526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-658-136-2

Query Match 5.0%; Score 44.8; DB 3; Length 53526;
Best Local Similarity 50.0%; Pred. No. 0.037;
Matches 112; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

553 CTTCGCAATTAAGCTATCTCTTAAACCTTCTCTCATTCCTGCTTTTATCTGAAC 612
3608 CTCCCTCTCTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 36067
613 CCGTAGGTGTCTCAATTAATTCCTGTCCTCTCTGAGATCATTAATGCTCTAC 672
3608 CCGTCCCT 36127
673 ATGGCCGTTTCT 732
36128 TTCTTCT 36187
733 GCCCAGCTACTCTCCAGCGGATCTCTGCTCCGCGGAGTCT 776
36188 CTCTCCCT 36231

RESULT 6
US-08-658-136-1
Sequence 1, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

RESULT 8
 US-08-510-646B-9
 ; Sequence 9, Application US/08510646B
 ; Patent No. 6077699
 ;
 ; GENERAL INFORMATION:
 ;
 APPLICANT: Blanc, Veronique
 APPLICANT: Blanche, Francis
 APPLICANT: Crouzet, Joel
 APPLICANT: Jacques, Nathalie

APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flumegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4000
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: S.pristinaespiralis
FEATURE:
NAME/KEY: CDS
LOCATION: 61..645
OTHER INFORMATION: /product= "gene papa"
US-08-510-646B-9

Query Match 4.9%; Score 43.8; DB 3; Length 645;
Best Local Similarity 46.1%; Pred. No. 0.0097;
Matches 185; Conservative 0; Mismatches 212; Indels 4; Gaps 1;

14 CCAGGACCCGAGATCAGCCGACCCGCTTTGGGGGCGAGTACATAGCATATCTCTCA 73
248 CCACCGACACCGACCTGGGCTTCAGCGCGCGGTGATCAGCAATGGAGACTGCGCTGC 307
74 ACTGGAAGCTCTCTGGGAGTCTGTGCTTTGCTGACACACGAGAGCATCTCAGGACG 133
308 TCGGGGTGTGCTGGGACACAGACCTGTGTCTGCTGCGGCGCCGCTGTCCACG 367
134 AGGGCAGCCCTCTCACCACCGCGCAGAGAGCAGAGAGGAGGCTCCCAACATTGC 193
368 CACCGAACCTTTTCAGGCGCGC---ACGAGCAGATCCGCGACGAGGCGAGGCGCTG 423

194 CTGAGGCCCCCGAGTCCCGGAGACCTTGGCCAGGGGACCCCTCTTTGAAGATC 253
424 TTGCGGAACATTCCTCTCCCGCTACCGTGTCCGCTACATGCTGACCGTCCGGCAA 483
254 CTCGCGTACCCCGCCGAGTGTCTCCCTGAGAGACCTGCTGAACATGAGCTTGGCCC 313
484 CTGCGCGCGACCTGGCGGCGACCGCCACACCGCGCAGCTGATGCGCGTCCG 543
314 CTGAACCGCTTAGAAGCGATTCCTCAACCTCCCGGCGCTGACGACCTTGGCGGAG 373
544 CACCGCACCTGCGCCCGCTTGGGCTGACAGTTCCACCCCAATGATCAGACGAGCAC 603
374 GACCCGAGCCCCCAGAAAACCCCTGCGCTGCGCCCTGAG 414
604 GGCACCGAGTGTCTGCGCACTTCGCGACCTGTCTTGGCG 644

RESULT 9
US-09-231-818-9
Sequence 9, Application US/09231818
Patent No. 6171846
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanchet, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flumegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,818
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4000
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA

HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: S.pristinaespiralis
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 61..645
 OTHER INFORMATION: /product= "gene papa"
 US-09-231-818-9

Query Match 4.9%; Score 43.8; DB 3; Length 645;
 Best Local Similarity 46.1%; Pred. No. 0.0097;
 Matches 185; Conservative 0; Mismatches 212; Indels 4; Gaps 1;

14 CCAGGACCCAGACTCAGCCCACTTTGGGGGCGATGATAGCATGATCTCA 73
 248 CCACGACACGACCTGGGCTTACCGCCCGGGTATATACCGAATGGACCTGCCGCTGC 307
 74 ACTGAAAGCTCTGGGGATCTGTGCTTTGCTTGCACACAGAGCATCTCAGGCACG 133
 308 TCGGGGTGTCTGGGCGACAGGCTGTGCTGTCTGCGCGCGCGCGCTGTCACG 367
 134 AGGGCACCCCTCTACCCACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 193
 368 CACCGAACCTTTTACGCGCGC---ACAGCGACATCCGCGACAGAGAGAGAGAGAG 423
 194 CTCAGAGGCCCCCACTCCCGGTGACCTTGGGCGACAGGCGACCCCTCTTTGAAGATC 253
 424 TTCGGAACATCTCCCTCCCGGTGACGTTGCGGTACCTGCTGATACCGTCCGCGCA 483
 254 CTCGGCCATACCGGCGCGCGGTGTCTGTGAAGAGAGAGAGAGAGAGAGAGAGAG 313
 484 CTGCGCGCGACCTGGGCGCGACCGCGCACCGCGAGCGAGCTGATGCGCGCGC 543
 314 CTGAACCCCTAGAGAGAGATCTCTCACTCCCGCGCTGAGAGAGAGAGAGAGAGAG 373
 544 CACCGCACCTGGCGCGCGGTGTGCTGTGATTCACCCCGAATGATGAGAGAGAGAG 603
 374 GACCCAGCCCCAG 414
 604 GCGCACCGAGATCTGCGCACTTCCGCGAGCTGTCTGCG 644

RESULT 10

US-09-635-359B-9

Sequence 9, Application US/09635359B
 Patent No. 6670157

GENERAL INFORMATION:

APPLICANT: Blanc, Veronique

Blanche, Veronique

Crouzet, Joel

Jacques, Nathalie

Lacroix, Patricia

Thibaut, Denis

Zagorec, Monique

Debusche, Laurent

De Crecy-Lagard, Valerie

Polypeptides Involved In The

Biosynthesis Of Streptogramins, Nucleotide Sequences

Coding For These Polypeptides And Their Use

CORRESPONDENCE ADDRESS:

ADDRESS: Flinagan, Henderson, Farabow, Garrett & Dunner

STREET: 1100 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/635,359B

FILING DATE: 09-Aug-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/231,818

FILING DATE: 15-JAN-1999

APPLICATION NUMBER: US 08/403,852

FILING DATE: 10-MAY-1995

APPLICATION NUMBER: PCT/FR 93/00923

FILING DATE: 25-SEP-1993

APPLICATION NUMBER: FR 92/11441

FILING DATE: 25-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 03806.0054-03000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 645 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: S.pristinaespiralis

FEATURE:

NAME/KEY: CDS

LOCATION: 61..645

OTHER INFORMATION: /product= "gene papa"

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-635-359B-9

Query Match 4.9%; Score 43.8; DB 4; Length 645;

Best Local Similarity 46.1%; Pred. No. 0.0097;

Matches 185; Conservative 0; Mismatches 212; Indels 4; Gaps 1;

14 CCAGGACCCAGACTCAGCCCACTTTGGGGGCGATGATAGCATGATCTCA 73
 248 CCACGACACGACCTGGGCTTACCGCCCGGGTATATACCGAATGGACCTGCCGCTGC 307
 74 ACTGAAAGCTCTGGGGATCTGTGCTTTGCTTGCACACAGAGCATCTCAGGCACG 133
 308 TCGGGGTGTCTGGGCGACAGGCTGTGCTGTCTGCGCGCGCGCGCTGTCACG 367
 134 AGGGCACCCCTCTACCCACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 193
 368 CACCGAACCTTTTACGCGCGC---ACAGCGACATCCGCGACAGAGAGAGAGAGAG 423
 194 CTCAGAGGCCCCCACTCCCGGTGACCTTGGGCGACAGGCGACCCCTCTTTGAAGATC 253
 424 TTCGGAACATCTCCCTCCCGGTGACGTTGCGGTACCTGCTGATACCGTCCGCGCA 483
 254 CTCGGCCATACCGGCGCGGTGTCTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 313
 484 CTGCGCGCGACCTGGGCGCGACCGCGCACCGCGAGCGAGCTGATGCGCGCGC 543
 314 CTGAACCCCTAGAGAGAGATCTCTCACTCCCGCGCTGAGAGAGAGAGAGAGAGAG 373
 544 CACCGCACCTGGCGCGCGGTGTGCTGTGATTCACCCCGAATGATGAGAGAGAGAG 603
 374 GACCCAGCCCCAG 414
 604 GCGCACCGAGATCTGCGCACTTCCGCGAGCTGTCTGCG 644

RESULT 11

US-09-249-585A-2/c

Sequence 2, Application US/09249585A

Patent No. 6417002
GENERAL INFORMATION:
APPLICANT: Horlick, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REFERENCE: 0867/0D905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 1926
TYPE: DNA
ORGANISM: Epstein Barr Virus
FEATURE:
NAME/KEY: CDS
LOCATION: (1) (1926)
OTHER INFORMATION: coding strand of EBNA-1 DNA
US-09-249-585A-2

Query Match 4.8%; Score 42.6; DB 4; Length 1926;
Best Local Similarity 43.6%; Pred. No. 0.035;
Matches 247; Conservative 0; Mismatches 314; Indels 6; Gaps 1;

QY 194 CTCAGGCCCCCGAGTCCCGGTGACCTTGGCCAGGCGGACCCCTCTCTTGAAGATC 253
DB CTCCTGCCCCCTCGCCCT 806
QY 254 CTCGGCTACCGGCGCCAGTGTCTCTGAGAGACCTGGAACCTGGAATCTGGCCCC 313
DB CCCCTCTGCCCCCT 746
QY 314 CTGAACCGCCTAGAACGAGATCTCTCAACCTCCCGGCTGAGACCTTGGCCGAG 373
DB CTCCTGCTCTGCCCCCT 686
QY 374 GACCCAGCCCCCGAAGAAACCCCTGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 427
DB CTCCTGCCCCCTCGCCCT 626
QY 428 CTCAGAGAGAGCGACGACTTGAACCCACCCCGGAGAGTACAGATTAAGATCTCCCTCA 487
DB CTCCTGCCCCCTCGCCCT 566
QY 488 GCGCTTCTGTCCAGGACATCTCCAGGACACGACCTCTCAACCTTGAATCTCCCGT 547
DB CTCCT 506
QY 548 GAATCTTCCCAATTAGACCTATCTCTTAAACCTCTCTCTCTCTCTCTCTCTCTCTCT 607
DB CCCCTCTGCCCCCTCGCCCT 446
QY 608 TGAACCGCTAGAGGAGTGTCTCAATATTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 667
DB CTCGCCCCCT 386
QY 668 CTCACATGCGCCGTTTCTCTCTGACGACCTTAACTCTCTCTCTCTCTCTCTCTCTCT 727
DB CTCCT 326
QY 728 CTTGAGGCCCACTTACTCTCCACCCGG 754
DB CCCCT 299

RESULT 12
US-09-410-399-3/c
Sequence 3, Application US/09410399
Patent No. 6482587
GENERAL INFORMATION:
APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
TITLE OF INVENTION: to Genomic Host DNA

FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1926
TYPE: DNA
ORGANISM: Epstein-Barr Virus
US-09-410-399-3

Query Match 4.8%; Score 42.6; DB 4; Length 1926;
Best Local Similarity 43.6%; Pred. No. 0.035;
Matches 247; Conservative 0; Mismatches 314; Indels 6; Gaps 1;

QY 194 CTCAGGCCCCCGAGTCCCGGTGACCCCTTGGCCAGGCGGACCCCTCTCTTGAAGATC 253
DB CTCCTGCCCCCTCGCCCT 806
QY 254 CTCGGCTACCGGCGCCAGTGTCTCTGAGAGACCTGGAACCTGGAATCTGGCCCC 313
DB CCCCTCTGCCCCCT 746
QY 314 CTGAACCGCCTAGAACGAGATCTCTCAACCTCCCGGCTGAGACCTTGGCCGAG 373
DB CTCCTGCTCTGCCCCCT 686
QY 374 GACCCAGCCCCCGAAGAAACCCCTGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 427
DB CTCCTGCCCCCTCGCCCT 626
QY 428 CTCAGAGAGAGCGACGACTTGAACCCACCCCGGAGAGTACAGATTAAGATCTCCCTCA 487
DB CTCCTGCTCTGCCCCCT 566
QY 488 GCGCTTCTGTCCAGGACATCTCCAGGACACGACCTCTCAACCTTGAATCTCCCGT 547
DB CTCCT 506
QY 548 GAATCTTCCCAATTAGACCTATCTCTTAAACCTCTCTCTCTCTCTCTCTCTCTCTCT 607
DB CCCCTCTGCCCCCTCGCCCT 446
QY 608 TGAACCGCTAGAGGAGTGTCTCAATATTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 667
DB CTCGCCCCCT 386
QY 668 CTCACATGCGCCGTTTCTCTCTGACGACCTTAACTCTCTCTCTCTCTCTCTCTCTCT 727
DB CTCCT 326
QY 728 CTTGAGGCCCACTTACTCTCCACCCGG 754
DB CCCCT 299

RESULT 13
US-09-050-863-2/c
Sequence 2, Application US/09050863
Patent No. 611411
GENERAL INFORMATION:
APPLICANT: Lao, Ying
APPLICANT: Hiang, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: Mammalian Protein Interaction Cloning
TITLE OF INVENTION: System
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Teet, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA

ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,863
FILING DATE: 30-MAR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 949-8711
TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
US-09-050-863-2

Query Match 4.8%; Score 42.6; DB 3; Length 2580;
Best Local Similarity 43.6%; Pred. No. 0.039;
Matches 247; Conservative 0; Mismatches 314; Indels 6; Gaps 1;
QY 194 CTCAGGGCCCCCAGTCCCGGTGACCTTGGCCAGGGGACCCCTCTTTGAAGATC 253
DB 1248 CTCCTGCCCCCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1189
QY 254 CTCGCGCTACCCGCGCCCACTGCTCCCTGAGAGAGACTGCTGAAGCTGAGTGGCCCC 313
DB 1188 CCCCCTGCGCCCT 1129
QY 314 CTGAACCCGCTGAAGAGGATCTCTCAACTCCCGGCGCTGAGACCTTTGGCGGAG 373
DB 1128 CTCCTGCTCTGCCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1069
QY 374 GACCCAGCCCCCAGAAAACCTGAGCTCTGCGCCCGAGAGTGAACCGA-----C 427
DB 1068 CTCCTGCCCCCT 1009
QY 428 CTCGAGAGAGCCAGACTAGACCCACCCCGGAGAGTACAGTAATGAGTCCCTCA 487
DB 1008 CTCCTGCCCCCT 949
QY 488 GCGCTTCTGTTCCAGGAGATCTCAGAGACCCAGCCCTCTCCACCTTGATTTCCCGT 547
DB 948 CTCCTCTCTGCTCTGCCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 889
QY 548 GAATCTTCCCAATTAGACCTATCTCTTAACCTCTTCTCAATCCCTGGTTTATTTC 607
DB 888 CCCCCTCTGCCCCCT 829
QY 608 TGAACCGCTAAGAGTGTCTCAATATTTCTGCTCTCTCTCTCTCTCTCTCTCTCT 667
DB 828 CTGCGCT 769
QY 668 CTGACATGCGCGTTTCTCTCTGACAGGCTAAGACTACTCTCTCACTCCGCTCTCAAG 727
DB 768 CTCCTCTCTGCTCTGCCCCCTCTGCCCCCTCTGCCCCCTCTGCCCCCTCTCTCTCT 709
QY 728 CTCGAGCCCACTACTCTCCACCCG 754
DB 708 CCCCCT 682

RESULT 14
US-09-359-081-2/c

Sequence 2, Application US/09359081
Patent No. 6316223
GENERAL INFORMATION:
APPLICANT: Lao, Ying
Huang, Betty
Payan, Don
TITLE OF INVENTION: Mammalian Protein Interaction Cloning
System
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,081
FILING DATE: 22-Jul-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/050,863
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 949-8711
TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-359-081-2

Query Match 4.8%; Score 42.6; DB 3; Length 2580;
Best Local Similarity 43.6%; Pred. No. 0.039;
Matches 247; Conservative 0; Mismatches 314; Indels 6; Gaps 1;
QY 194 CTCAGGGCCCCCAGTCCCGGTGACCTTGGCCAGGGGACCCCTCTTTGAAGATC 253
DB 1248 CTCCTGCCCCCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1189
QY 254 CTCGCGCTACCCGCGCCCACTGCTCCCTGAGAGAGACTGCTGAAGCTGAGTGGCCCC 313
DB 1188 CCCCCTGCGCCCT 1129
QY 314 CTGAACCCGCTGAAGAGGATCTCTCAACTCCCGGCGCTGAGACCTTTGGCGGAG 373
DB 1128 CTCCTGCTCTGCCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1069
QY 374 GACCCAGCCCCCAGAAAACCTGAGCTCTGCGCCCGAGAGTGAACCGA-----C 427
DB 1068 CTCCTGCCCCCT 1009
QY 428 CTCGAGAGAGCCAGACTAGACCCACCCCGGAGAGTACAGTAATGAGTCCCTCA 487
DB 1008 CTCCTGCCCCCT 949
QY 488 GCGCTTCTGTTCCAGGAGATCTCAGGACCCAGCCCTCTCCACCTTGATTTCCCGT 547
DB 948 CTCCTCTCTGCTCTGCCCCCTCTGCCCCCTCTGCCCCCTCTGCCCCCTCTCTCTCT 889

```

Qy 548 GAATCTTCCCAATTAGACCTATCTCTTAACCTCTTCTCATTTCCGTTTATTC 607
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 888 CCCCCTGCCCCCTCCGCCCCCTCTCTCTCTGCCCCCTCCGCCCCCTCTCTGTC 829
Qy 608 TGAACCCGTAAGTGTTCTCAATATTTCTCTCTCTCTCTCTCTCTCTCTCTCT 667
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 828 CTGCCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 769
Qy 668 CTGACATGCCCCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 727
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 768 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 709
Qy 728 CCTGAGCCCCCACTACCTCCACCCCG 754
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 708 CCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 682

```

```

RESULT 15
US-09-130-114-1
; Sequence 1, Application US/09130114
; Patent No. 5976807
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert A.
; APPLICANT: Dama, Basam B.
; APPLICANT: Robbins, Alan K.
; TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
; FILE REFERENCE: 0867/ID903US1
; CURRENT APPLICATION NUMBER: US/09/130,114
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 5452
; TYPE: DNA
; ORGANISM: VEBNA
US-09-130-114-1

```

```

Query Match 4.88; Score 42.6; DB 2; Length 5452;
Best Local Similarity 43.68; Pred. No. 0.055;
Matches 247; Conservative 0; Mismatches 314; Indels 6; Gaps 1;

```

```

Qy 194 CTCAGGCCCCCGAGTCCCGGAGTCCGAGCCCTTGGCCAGGCGACCCCTCTTTGAAGATC 253
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1557 CTCCTGCCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1616
Qy 254 CTCGCGCTACCCCGCCGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 313
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1617 CCCCCTCTGCCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1676
Qy 314 CTGAACCGCTAGAGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 373
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1677 CTCCTGCTCTGCCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1736
Qy 374 GACCCGAGCCCCGAGAAACCCCTGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 427
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1737 CTCCTGCCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1796
Qy 428 CTCAGAGAGCCGAGACTTACCCACCCCGGAGAGTACAGATTAAGAGTCCCTCA 487
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1797 CTCCTGCCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1856
Qy 488 GCGCTTCTGTTCCAGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 547
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1857 CTCCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1916
Qy 548 GAATCTTCCCAATTAGACCTATCTCTTAACCTCTTCTCTCTCTCTCTCTCTCTCTCT 607
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1917 CCCCCTCTGCCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1976
Qy 608 TGAACCCGTAAGTGTTCTCAATATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 667
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1977 CTGCCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2036

```

```

Qy 668 CTGACATGCCCCCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 727
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2037 CTCCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2096
Qy 728 CCTGAGCCCCCACTACCTCCACCCCG 754
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2097 CCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2123

```

Search completed: January 11, 2005, 09:15:02
Job time : 115 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: January 11, 2005, 06:59:39 ; Search time 596 Seconds
(without alignments)
8577.830 Million cell updates/sec

Title: US-09-994-365-1

Perfect score: 1 ccccttgggggtcccgagca.....taaaatcatgtttcttaa 891

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4293498 seqs, 2868903791 residues

Total number of hits satisfying chosen parameters: 8586996

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEM_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEM_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEM_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEM_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEM_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US11_NEM_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US11_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US60_NEM_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	891	100.0	891	9	US-09-994-365-1
2	775.4	87.0	2997	9	US-09-994-365-10
3	775.4	87.0	3001	9	US-09-994-365-4
4	775	87.0	55050	17	US-10-467-752-4
5	773.8	86.8	25235	15	US-10-164-230-2
6	563.4	63.2	565	15	US-10-029-386-5700
7	557.8	62.6	3673778	15	US-10-312-841-1
8	348.2	39.1	3673778	15	US-10-029-386-19510
9	157	17.6	157	15	US-10-017-161-1483
10	61.8	6.9	3133	15	US-10-017-161-1483
11	61.8	6.9	3133	15	US-10-292-798-1191
12	60	6.7	60	10	US-09-908-975-5077

13	56.6	6.4	925	17	US-10-437-963-44536	Sequence 44536, A
14	56	6.3	891	18	US-10-425-115-146045	Sequence 146045, A
15	52.8	5.9	5452	15	US-10-017-161-1481	Sequence 1481, Ap
16	52.8	5.9	5452	15	US-10-292-798-1189	Sequence 1189, Ap
17	51.8	5.8	671	14	US-10-184-644-346	Sequence 346, App
18	51.8	5.8	671	14	US-10-184-644-346	Sequence 346, App
19	51.8	5.8	959	17	US-10-437-963-48694	Sequence 48694, A
20	51.8	5.8	12733	14	US-10-032-393-47	Sequence 47, Appl
21	51.8	5.8	12739	14	US-10-032-393-8	Sequence 8, Appl
22	50.4	5.7	3163	15	US-10-017-161-1857	Sequence 1857, Ap
23	50.4	5.7	3163	15	US-10-292-798-1513	Sequence 1513, Ap
24	50	5.6	50	16	US-10-131-827-532	Sequence 532, App
25	49.2	5.5	942	18	US-10-425-115-22795	Sequence 22795, A
26	47.8	5.4	673	18	US-10-425-115-11145	Sequence 11145, A
27	47	5.3	1064	9	US-09-804-682-29	Sequence 29, Appl
28	46.6	5.2	629	17	US-10-021-323-9375	Sequence 9375, Ap
29	46.6	5.2	1117	15	US-10-017-161-1403	Sequence 1403, Ap
30	46.6	5.2	1117	15	US-10-292-798-1141	Sequence 1141, Ap
31	46	5.2	822	18	US-10-425-115-102047	Sequence 102047, A
32	45.4	5.1	3594	17	US-10-437-963-51978	Sequence 51978, A
33	45.2	5.1	694	14	US-10-184-644-60	Sequence 60, Appl
34	45.2	5.1	694	14	US-10-184-644-60	Sequence 60, Appl
35	45.2	5.1	712	18	US-10-425-115-118813	Sequence 118813, A
36	45	5.1	706	17	US-10-437-963-17102	Sequence 17102, A
37	45	5.1	805	16	US-10-424-599-61903	Sequence 61903, A
38	45	5.1	1327	17	US-10-437-963-40850	Sequence 40850, A
39	44.8	5.0	1327	16	US-10-398-221-1265	Sequence 1265, Ap
40	44.8	5.0	1732	17	US-10-437-963-77232	Sequence 77232, A
41	44.8	5.0	53522	10	US-09-904-968A-1	Sequence 1, Appl
42	44.6	5.0	497	16	US-10-424-599-13788	Sequence 13788, A
43	44.4	5.0	766	18	US-10-425-115-82176	Sequence 82176, A
44	44.4	5.0	862	17	US-10-437-963-28390	Sequence 28390, A
45	44.2	5.0	556	18	US-10-363-345A-23585	Sequence 23585, A

ALIGNMENTS

RESULT 1
US-09-994-365-1
Sequence 1, Application US/0994365
Patent No. US20020115148A1
GENERAL INFORMATION:
APPLICANT: Charmley, Patrick
APPLICANT: Moes, Patrick
APPLICANT: McEuen, Mark
TITLE OR INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
FILE REFERENCE: CECH118109
CURRENT APPLICATION NUMBER: US/09/994,365
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: US 60/253,592
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/256,839
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 891
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (64)..(471)
US-09-994-365-1

Query Match 100.0%; Score 891; DB 9; Length 891;
Best Local Similarity 100.0%; Pred. No. 3.4e-258;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ccccttgggggttcccgagcaccgagctcagccacccagctttgggggagccagctacata 60
Db 1 ccccttgggggttcccgagcaccgagctcagccacccagctttgggggagccagctacata 60

```
QY 61 GCGATGATCTCTCACTGTAAGCTCTTGAGGATCTGCTGCTTTGCTTGCACACACAGAGGC 120
D 61 GCGATGATCTCTCACTGTAAGCTCTTGAGGATCTGCTGCTTTGCTTGCACACAGAGGC 120
QY 121 ATCTCAGGACGAGGAGCCACCCCTCTCACCACCCGACAGAGAGAGAGAGAGAGGC 180
D 121 ATCTCAGGACGAGGAGCCACCCCTCTCACCACCCGACAGAGAGAGAGAGAGAGGC 180
QY 181 TCCCAACATTGCTCTGAGGAGCCCGGAGTCCCGGTAACCTTGGCCAGAGAGAGAGGC 240
D 181 TCCCAACATTGCTCTGAGGAGCCCGGAGTCCCGGTAACCTTGGCCAGAGAGAGAGGC 240
QY 241 CTCTTTAAGATCTCTCGGCTTACCGGCTTACCGGCTTACCGGCTTACCGGCTTAC 300
D 241 CTCTTTAAGATCTCTCGGCTTACCGGCTTACCGGCTTACCGGCTTACCGGCTTAC 300
QY 301 GAGATCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAG 360
D 301 GAGATCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAG 360
QY 361 CTTTGGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
D 361 CTTTGGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 AACGACCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
D 421 AACGACCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 CCGCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAG 540
D 481 CCGCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAG 540
QY 541 TCCCGGAGATCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAG 600
D 541 TCCCGGAGATCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAG 600
QY 601 TTATATCTGAACCCGTAAGGAGTGTCTCAATATTTCTGATCTCTGATCTCTGATCT 660
D 601 TTATATCTGAACCCGTAAGGAGTGTCTCAATATTTCTGATCTCTGATCTCTGATCT 660
QY 661 CTTAGTCTCAGATGCGCCGCTTTTCTCTGACAGGCTTACCTTCTCTGATCTCTGAT 720
D 661 CTTAGTCTCAGATGCGCCGCTTTTCTCTGACAGGCTTACCTTCTCTGATCTCTGAT 720
QY 721 CTCAGGCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCT 780
D 721 CTCAGGCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCT 780
QY 781 CAGGCTATGATGTAATGATGTTCCCTTCTGACAGGCTTACCTTCTCTGATCTCTGAT 840
D 781 CAGGCTATGATGTAATGATGTTCCCTTCTGACAGGCTTACCTTCTCTGATCTCTGAT 840
QY 841 AGACAGCTGCTCTTCTTCAATGAAAGGAAATTAATATCATGTTTCTTAA 891
D 841 AGACAGCTGCTCTTCTTCAATGAAAGGAAATTAATATCATGTTTCTTAA 891

RESULT 2
US-09-994-365-10
; Sequence 10, Application US/09994365
; Patent No. US20020115148A1
; GENERAL INFORMATION:
; APPLICANT: Charmley, Patrick
; APPLICANT: Moss, Patrick
; APPLICANT: McEwen, Mark
; TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
; FILE REFERENCE: CECH18109
; CURRENT APPLICATION NUMBER: US/09/994,365
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 60/253,592
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/256,839
; PRIOR FILING DATE: 2000-12-15
```

```
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10
LENGTH: 2997
TYPE: DNA
ORGANISM: Homo sapiens
US-09-994-365-10

Query Match      87.0%; Score 775.4; DB 9; Length 2997;
Best Local Similarity 99.9%; Pred. No. 3.4e-223;
Matches 776; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 115 AGAGGATCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 174
D 115 AGAGGATCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 174
QY 175 GAGAGCTCTCCCAATTTGCTCTGAGGAGCCCGGAGTCCCGGTAACCTTGGCCAGAGAG 234
D 175 GAGAGCTCTCCCAATTTGCTCTGAGGAGCCCGGAGTCCCGGTAACCTTGGCCAGAGAG 234
QY 2258 GAGAGCTCTCCCAATTTGCTCTGAGGAGCCCGGAGTCCCGGTAACCTTGGCCAGAGAG 2317
D 2258 GAGAGCTCTCCCAATTTGCTCTGAGGAGCCCGGAGTCCCGGTAACCTTGGCCAGAGAG 2317
QY 235 CCGCTCTCTTTGAAGATCTCTCGGCTTACCGGCTTACCGGCTTACCGGCTTACCGGCT 294
D 235 CCGCTCTCTTTGAAGATCTCTCGGCTTACCGGCTTACCGGCTTACCGGCTTACCGGCT 294
QY 2318 CCGCTCTCTTTGAAGATCTCTCGGCTTACCGGCTTACCGGCTTACCGGCTTACCGGCT 2377
D 2318 CCGCTCTCTTTGAAGATCTCTCGGCTTACCGGCTTACCGGCTTACCGGCTTACCGGCT 2377
QY 295 GAAACTGAGATCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCT 354
D 295 GAAACTGAGATCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCT 354
QY 335 GAGAGCTCTTGGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 414
D 335 GAGAGCTCTTGGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 414
QY 2438 GAGAGCTCTTGGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2497
D 2438 GAGAGCTCTTGGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2497
QY 415 GTGAGCAACCGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 474
D 415 GTGAGCAACCGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 474
QY 2498 GTGAGCAACCGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2557
D 2498 GTGAGCAACCGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2557
QY 475 TGAAGTCCCTCAGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCT 534
D 475 TGAAGTCCCTCAGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCT 534
QY 535 TCGATTTCCCGGAGATCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCT 594
D 535 TCGATTTCCCGGAGATCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCT 594
QY 2618 TCGATTTCCCGGAGATCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCT 2677
D 2618 TCGATTTCCCGGAGATCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCT 2677
QY 595 CTGAGTTTATTTGAGAACCCGTAAGGAGTGTCTCAATATTTCTGATCTCTGATCTCTGAT 654
D 595 CTGAGTTTATTTGAGAACCCGTAAGGAGTGTCTCAATATTTCTGATCTCTGATCTCTGAT 654
QY 2678 CTGAGTTTATTTGAGAACCCGTAAGGAGTGTCTCAATATTTCTGATCTCTGATCTCTGAT 2737
D 2678 CTGAGTTTATTTGAGAACCCGTAAGGAGTGTCTCAATATTTCTGATCTCTGATCTCTGAT 2737
QY 655 TCCATATCTAGTCTCAGATGCGCCGCTTTTCTCTGACAGGCTTACCTTCTCTGATCTCTGAT 714
D 655 TCCATATCTAGTCTCAGATGCGCCGCTTTTCTCTGACAGGCTTACCTTCTCTGATCTCTGAT 714
QY 715 CCGCTCTCAGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAG 774
D 715 CCGCTCTCAGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAG 774
QY 2798 CCGCTCTCAGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAG 2857
D 2798 CCGCTCTCAGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAG 2857
QY 775 CTGAGGAGAGGCTATGATGTAATGATGTTCCCTTCTGACAGGCTTACCTTCTCTGATCTCTGAT 834
D 775 CTGAGGAGAGGCTATGATGTAATGATGTTCCCTTCTGACAGGCTTACCTTCTCTGATCTCTGAT 834
QY 2858 CTGAGGAGAGGCTATGATGTAATGATGTTCCCTTCTGACAGGCTTACCTTCTCTGATCTCTGAT 2917
D 2858 CTGAGGAGAGGCTATGATGTAATGATGTTCCCTTCTGACAGGCTTACCTTCTCTGATCTCTGAT 2917
QY 835 ATCAGTGAAGAGCTGCTCTTCAATGAAAGGAAATTAATATCATGTTTCTTAA 891
D 835 ATCAGTGAAGAGCTGCTCTTCAATGAAAGGAAATTAATATCATGTTTCTTAA 891
QY 2918 ATCAGTGAAGAGCTGCTCTTCAATGAAAGGAAATTAATATCATGTTTCTTAA 2974
D 2918 ATCAGTGAAGAGCTGCTCTTCAATGAAAGGAAATTAATATCATGTTTCTTAA 2974

RESULT 3
US-09-994-365-4
; Sequence 4, Application US/09994365
; Patent No. US20020115148A1
; GENERAL INFORMATION:
; APPLICANT: Charmley, Patrick
; APPLICANT: Moss, Patrick
; APPLICANT: McEwen, Mark
```


;; TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
;; FILE REFERENCE: CECH118109
;; CURRENT APPLICATION NUMBER: US/09/994,365
;; PRIORITY FILING DATE: 2001-11-26
;; PRIOR APPLICATION NUMBER: US 60/253,592
;; PRIOR FILING DATE: 2000-11-28
;; PRIOR APPLICATION NUMBER: US 60/256,839
;; PRIOR FILING DATE: 2000-12-15
;; NUMBER OF SEQ ID NOS: 16
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 4
;; LENGTH: 3001
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; US-09-994-365-4

Query Match 87.0%; Score 775.4; DB 9; Length 3001;
Best Local Similarity 99.9%; Pred. No. 3,4e-223;
Matches 776; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 115 AGAGGATCTCAGGACGAGGAGGACCCCTCTGACCAACCCGAGAGAGACCGAGAGAG 174
DB 2202 ACAGGATCTCAGGACGAGGAGGACCCCTCTGACCAACCCGAGAGAGAGAGAGAG 2261
QY 175 GCAGGCTCCCCAATTGCTCAGAGGCCCCCAGTCCCGGTGACCTTGCGCAGGAGCA 234
DB 2262 GCAGGCTCCCCAATTGCTCAGAGGCCCCCAGTCCCGGTGACCTTGCGCAGGAGCA 2321
QY 235 CCCCCTCTTTGAGATCTCCGCTACCCGCGCAGTGTCTCTGAGAGACCTGCT 294
DB 2322 CCCCCTCTTTGAGATCTCCGCTACCCGCGCAGTGTCTCTGAGAGACCTGCT 2381
QY 295 GAAACTGAGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 354
DB 2382 GAAACTGAGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2441
QY 355 GAGGACCTTGGCGGAGAGACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 414
DB 2442 GAGGACCTTGGCGGAGAGACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2501
QY 415 GTGAGCAACGAGCTCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 474
DB 2502 GTGAGCAACGAGCTCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2561
QY 475 TGAAGTCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 534
DB 2562 TGAAGTCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2621
QY 535 TCGAATCCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 594
DB 2622 TCGAATCCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2681
QY 595 CTCGGTTTATTCGAAACCGGTAAGGTGTGTCTCAATATTTCTGTCCCTCTGAGA 654
DB 2682 CTCGGTTTATTCGAAACCGGTAAGGTGTGTCTCAATATTTCTGTCCCTCTGAGA 2741
QY 655 TCCATATTAGTCTCTCATATGCCCCGTTTTTCTCTGAGAGGCTTAAGCTTCTCTCTA 714
DB 2742 TCCATATTAGTCTCTCATATGCCCCGTTTTTCTCTGAGAGGCTTAAGCTTCTCTA 2801
QY 715 CCTGCGCTCAGAGGCTGAGGCCCCCAGCTACCTCCAGCCGGCTTCTGTCCCGCGAGTGC 774
DB 2802 CCTGCGCTCAGAGGCTGAGGCCCCCAGCTACCTCCAGCCGGCTTCTGTCCCGCGAGTGC 2861
QY 775 CTGCGGAGGAGGCTATGATCTGTCTCTCTCTGAGGAGGAGGAGGAGGAGGAGGAG 834
DB 2862 CTGCGGAGGAGGCTATGATCTGTCTCTCTCTGAGGAGGAGGAGGAGGAGGAGGAG 2921
QY 835 ATCAGTGAAGAGCTGCTCTCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 891
DB 2922 ATCAGTGAAGAGCTGCTCTCTCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2978

RESULT 4
US-10-467-752-4
;; Sequence 4, Application US/10467752
;; Publication No. US20040161759A1
;; GENERAL INFORMATION:
;; APPLICANT: Lemch, et al.
;; TITLE OF INVENTION: Test and Model for Inflammatory disease
;; FILE REFERENCE: 2003882-0009
;; CURRENT APPLICATION NUMBER: US/10/467,752
;; CURRENT FILING DATE: 2003-08-13
;; PRIOR APPLICATION NUMBER: PCT/GB02/00653
;; PRIOR FILING DATE: 2002-02-13
;; PRIOR APPLICATION NUMBER: GB0103514.6
;; PRIOR FILING DATE: 2001-02-13
;; NUMBER OF SEQ ID NOS: 109
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 4
;; LENGTH: 55050
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURES:
;; NAME/KEY: misc_feature
;; LOCATION: (13351)..(13351)
;; OTHER INFORMATION: n is a or t or g or c
;; NAME/KEY: misc_feature
;; LOCATION: (13401)..(13401)
;; OTHER INFORMATION: n is a or t or g or c
;; US-10-467-752-4

Query Match 87.0%; Score 775; DB 17; Length 55050;
Best Local Similarity 99.7%; Pred. No. 9,4e-223;
Matches 775; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 115 AGAGGATCTCAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 174
DB 27096 ACAGGATCTCAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 27155
QY 175 GCAGGCTCCCCAATTGCTCAGAGGCCCCCAGTCCCGGTGACCTTGCGCAGGAGCA 234
DB 27156 GCAGGCTCCCCAATTGCTCAGAGGCCCCCAGTCCCGGTGACCTTGCGCAGGAGCA 27215
QY 235 CCCCCTCTTTGAGATCTCCGCTACCCGCGCAGTGTCTCTGAGAGACCTGCT 294
DB 27216 CCCCCTCTTTGAGATCTCCGCTACCCGCGCAGTGTCTCTGAGAGACCTGCT 27275
QY 295 GAAACTGAGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 354
DB 27276 GAAACTGAGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 27335
QY 355 GAGGACCTTGGCGGAGAGACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 414
DB 27336 GAGGACCTTGGCGGAGAGACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 27395
QY 415 GTGAGCAACGAGCTCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 474
DB 27396 GTGAGCAACGAGCTCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 27455
QY 475 TGAAGTCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 534
DB 27456 TGAAGTCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 27515
QY 535 TCGAATCCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 594
DB 27516 TCGAATCCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 27575
QY 595 CTCGGTTTATTCGAAACCGGTAAGGTGTGTCTCAATATTTCTGTCCCTCTGAGA 654
DB 27576 CTCGGTTTATTCGAAACCGGTAAGGTGTGTCTCAATATTTCTGTCCCTCTGAGA 27635
QY 655 TCCATATTAGTCTCTCATATGCCCCGTTTTTCTCTGAGAGGCTTAAGCTTCTCTCTA 714
DB 27636 TCCATATTAGTCTCTCATATGCCCCGTTTTTCTCTGAGAGGCTTAAGCTTCTCTCTA 27695

QY	715	CCTGGCCCTCCAGGCGCTCGGCCCCCACTCACTCCACCCGGGTCTTCTGCCCCGGCAGATG	774
Db	27686	CCTGGCCCTCCAGGCGCTCGGCCCCCACTCACTCCACCCGGGTCTTCTGCCCCGGCAGATG	27755
QY	775	CTGGGGCAGGGCTATNGTACTGTTGCTTCCCTTCTGCGCACTGTGTGGCCCCGGCAGGAAGT	834
Db	27756	CTGGGGCAGGGCTATNGTACTGTTGCTTCCCTTCTGCGCACTGTGTGGCCCCGGCAGGAAGT	27815
QY	835	ATCATGTACACAGCTGTGCTGCTTCCATGAAACGAAAAATATAAAATCATGTTTCTTAA	891
Db	27816	ATCATGTACACAGCTGTGCTGCTTCCATGAAACGAAAAATATAAAATCATGTTTCTTAA	27872

```

RESULT 5
US-10-164-230-2
; Sequence 2, Application US/10164230
; Publication No. US2003017065A1
; GENERAL INFORMATION:
; APPLICANT: Inoko, Hidetoshi
; APPLICANT: Tamaiya, Gen
; TITLE OF INVENTION: METHOD OF TESTING FOR PSORIASIS VULGARIS
; FILE REFERENCE: 06501-112U51
; CURRENT APPLICATION NUMBER: US/10/164,230
; PRIOR FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: PCT/JP00/08624
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: JP 11/346867
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 2

```

```

? LENGTH: 25235
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: exon
? LOCATION: (1)...(420)
? FEATURE:
? NAME/KEY: exon
? LOCATION: (1282)...(1405)
? FEATURE:
? NAME/KEY: exon
? LOCATION: (1602)...(1702)
? FEATURE:
? NAME/KEY: exon
? LOCATION: (1602)...(1631)
? FEATURE:
? NAME/KEY: exon
? LOCATION: (2352)...(2364)
? FEATURE:
? NAME/KEY: exon
? LOCATION: (6287)...(6509)
? FEATURE:
? NAME/KEY: exon
? LOCATION: (10417)...(10493)
? FEATURE:
? NAME/KEY: exon
? LOCATION: (14244)...(14407)
? FEATURE:
? NAME/KEY: exon
? LOCATION: (14244)...(14344)
? FEATURE:
? NAME/KEY: exon
? LOCATION: (25190)...(25235)
? OS-10-164-230-2

```

Query Match	86.8%	Score 773.8	DB 15	Length 25235
Best Local Similarity	99.7%	Pred. No. 1.8e-222		
Matches 775; Conservative	0	Mismatches 2	Indels 0	Gaps 0

115 AGAGGATCTCAGGCAAGGAGGCCACCCCTCTACCCACCCGACAGAGACCGAGAGAG 174

Dp	1751	ACAGGACTTCCAGGCAGGAGGCGCACCCCTCTCACCACCCGACAGAGACCGGAGAG	1810
Qy	175	GCAGGCTTCCCOAACATTGGCTTCAAGGGCCCCCAGTCCCGGTGACACCTTGGCCAGGAGCA	234
Dp	1811	GCAGGCTTCCCOAACATTGGCTTCAAGGGCCCCCAGTCCCGGTGACACCTTGGCCAGGAGCA	1870
Qy	235	CCCCCTCTTTTAAAGATCTCCGCGCTAACCCGCGCCAGTGTCTCCCTGGAGAGACTGTGCTT	294
Dp	1871	CCCCCTCTCTTTAAAGATCTCCGCGCTAACCCGCGCCAGTGTCTCCCTGGAGAGACTGTGCTT	1930
Qy	295	GAAACTGGAATCTGGCCCCCTGAAACCGCTAAGACCGATCTCTCAACCTCCCGGCT	354
Dp	1931	GAAACTGGAATCTGGCCCCCTGAAACCGCTAAGACCGATCTCTCTCAACCTCCCGGCT	1990
Qy	355	GACGACCTTTGGCCGCGCAGACCCCGAGCCCCGAGAAAACCCCTGGCTCTCTCCCTGAG	414
Dp	1991	GACGACCTTTGGCCGCGCGCAGACCCCGAGCCCCGAGAAAACCCCTGGCTCTCTCCCTGAG	2050
Qy	415	GTGGACAAACCGACTCTCAGAGGAGCGACCTAAGACCAACCCCGGAGAGATCAGATTA	474
Dp	2051	GTGGACAAACCGACTCTCAGAGGAGCGACCTAAGACCAACCCCGGAGAGATCAGATTA	2110
Qy	475	TGGAGTCCCTCAGCCGTTCTGTCCAGGCACTCCCGAGGACCCAGCCCTCTCCACC	534
Dp	2111	TGGAGTCCCTCAGCCGTTCTGTCCAGGCACTCCCGAGGACCCAGCCCTCTCCACC	2170
Qy	535	TCTGATTCCTCGTAATCTTCCCAATTAGCCTATCTCTTAAACCTCTCTCATTTCC	594
Dp	2171	TCTGATTCCTCGTAATCTTCCCAATTAGCCTATCTCTTAAACCTCTCTCATTTCC	2230
Qy	595	CTCGGTTTAAATCTGAACCCCGTAGGTGTCTGCAATTTCTCTGTCCTCCCTCTGAGA	654
Dp	2231	CTCGGTTTAAATCTGAACCCCGTAGGTGTGTCTCAATTTCTCTGTCCTCCCTCTGAGA	2290
Qy	655	TCCAACTTAATGCTCCAGATGCCCCGTTTTTCTCTGACAGCCTAAGCCTACTCTCTTA	714
Dp	2291	TCCAACTTAATGCTCCAGATGCCCCGTTTTTCTCTGACAGCCTAAGCCTACTCTCTTA	2350
Qy	715	CCTGCGCTCCAGGCGCTCGGCCCACTACCTCCACCCCGGCTTCCGACCCGCGGACTG	774
Dp	2351	CCTGCGCTCCAGGCGCTCGGCCCACTACCTCCACCCCGGCTTCTCTGACCCGCGGACTG	2410
Qy	775	CTGGGGGAGGGCTATGCTATCTGTCTTCCCTTCTGCACTGTGTGCGCGCGGAGAGAACT	834
Dp	2411	CTGGGGGAGGGCTATGCTATCTGTCTTCCCTTCTGCACTGTGTGCGCGCGGAGAGAACT	2470
Qy	835	ATCAGTAGACAGCTGCTGTCTTCATGAAACGAAAAATAAAAATCAATGTTTCTTAA	891
Dp	2471	ATCAGTAGACAGCTGCTGTCTTCATGAAACGAAAAATAAAAATCAATGTTTCTTAA	2527

```

RESULT 6
US-10-029-386-5700
? Sequence 5700, Application US/10029386
? Publication No. US20030194704A1
? GENERAL INFORMATION:
? APPLICANT: Penn, Sharon G.
? APPLICANT: Rank, David R.
? APPLICANT: Hanzel, David K.
? TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GEN
? FILE OF INVENTION: EXPRESSION ANALYSIS TWO
? FILE REFERENCE: AEOMICA-X-2
? CURRENT APPLICATION NUMBER: US/10/029,386
? CURRENT FILING DATE: 2001-12-20
? NUMBER OF SEQ ID NOS: 34288
? SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
? SEQ ID NO 5700
? LENGTH: 565
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: MAP TO AB023060.1
? OTHER INFORMATION: EXPRESSED IN PLACENTA SIGNAL = 1

```

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.82
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.82
 OTHER INFORMATION: SWISSPROT HIT: O99715, EVALU6 6.20e-01
 OTHER INFORMATION: EST_HUMAN HIT: BF513178.1, EVALU6 0.00e+00
 OTHER INFORMATION: NT HIT: g115304354, EVALU6 0.00e+00
 US-10-029-386-5700

Query Match 63.2%; Score 563.4; DB 15; Length 565;
 Best Local Similarity 99.8%; Pred. No. 1.9e-159;
 Matches 564; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 235 CCCCCTCTTTGAAGATCCCTCCGCTACCCGCCCACTGCTCCCTGAGAGACCTGCT 294
 DB 1 CCCCCTCTCTTTGAAGATCCCTCCGCTACCCGCCCACTGCTCCCTGAGAGACCTGCT 60
 QY 295 GAAACTGGAAGTCTGCCCCCTGAAACCGCTTGAACGATCTCTCAACTCTCCCGGCT 354
 DB 61 GAAACTGGAAGTCTGCCCCCTGAAACCGCTTGAACGATCTCTCAACTCTCCCGGCT 120
 QY 355 GAGACCTCTTGAGCGGAGAGACCCAGGCCCCAGAAAAACCCCTGAGCCCTGAGCCCTGAG 414
 DB 121 GAGACCTCTTGAGCGGAGAGACCCAGGCCCCAGAAAAACCCCTGAGCCCTGAGCCCTGAG 180
 QY 415 GTGACAACCGACCTCAAGAGAGACCACTAGACCAACCCCGGAAAGATACAGATTA 474
 DB 181 GTGACAACCGACCTCAAGAGAGACCACTAGACCAACCCCGGAAAGATACAGATTA 240
 QY 475 TGAAGTCCCTCAGCCGCTCTGTTCCCAAGCATCTCCAGGACCAACCGCTCTCCACCC 534
 DB 241 TGAAGTCCCTCAGCCGCTCTGTTCCCAAGCATCTCCAGGACCAACCGCTCTCCACCC 300
 QY 535 TCTGATTCGCCGTAATCTTCCCAATTAGCTATCTCTTAAACCTCTTCAATTC 594
 DB 301 TCTGATTCGCCGTAATCTTCCCAATTAGCTATCTCTTAAACCTCTTCAATTC 360
 QY 595 CTCGGTTTATTCGAAACCGGTAAAGTGCTGTCTCAATATTCCTGCTCCCTGAGA 654
 DB 361 CTCGGTTTATTCGAAACCGGTAAAGTGCTGTCTCAATATTCCTGCTCCCTGAGA 420
 QY 655 TCCATCTTACTAGTCTCATATGCCCCGTTTTTCTCTGACAGCTTAAGCTACTCTCTA 714
 DB 421 TCCATCTTACTAGTCTCATATGCCCCGTTTTTCTCTGACAGCTTAAGCTACTCTCTA 480
 QY 715 CTCGCTCCAGAGCTCGGCCCCCACTACCTCCACCGGCTTCTGCGCGGAGATCG 774
 DB 481 CTCGCTCCAGAGCTCGGCCCCCACTACCTCCACCGGCTTCTGCGCGGAGATCG 540
 QY 775 CTGGGGCAGGCTATGCTACTGTGT 799
 DB 541 CTGGGGCAGGCTATGCTACTGTGT 565

RESULT 7

US-10-312-841-1/c
 ; Sequence 1, Application US/10312841
 ; Publication No. US20030186277A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Epigenomics AG
 ; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
 ; FILE REFERENCE: B01/1208/WO
 ; CURRENT APPLICATION NUMBER: US/10/312, 841
 ; CURRENT FILING DATE: 2002-12-30
 ; NUMBER OF SEQ ID NOS: 2
 ; SEQ ID NO 1
 ; LENGTH: 3673778
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
 ; NAME/KEY: unsure
 ; LOCATION: (3294164)
 ; US-10-312-841-1

Query Match 62.6%; Score 557.8; DB 15; Length 3673778;
 Best Local Similarity 82.4%; Pred. No. 9e-157;
 Matches 640; Conservative 0; Mismatches 137; Indels 0; Gaps 0;

QY 115 AGAGCATCTTCAGGACGAGAGGACCCCTCTGACCCACCCGAGAGAGACGAGAGAG 174
 DB 1426053 ACAAACTTCTCAACCAAGAAAACCCCTCTGACCCACCCGAGAGAGAGAGAGAG 1425994
 QY 175 GCAGGCTCCCAATTTGCTCAGAGGCCCCCACTGCTCCCGGTGACCTTGGCCAGGGCA 234
 DB 1425993 ACAAACTTCTCAACCAATTAACCTCAAAACCCCAATCCCGGTGACCTTGAACAAAACA 1425934
 QY 235 CCCCCTCTTTGAAGATCCCTCCGCTACCCGCCCACTGCTCCCTGAGAGACCTGCT 294
 DB 1425933 CCCCCTCTTTGAAGATCCCTCCGCTACCCGCCCACTGCTCCCTGAGAGACCTGCT 1425874
 QY 295 GAAACTGGAAGTCTGCCCCCTGAAACCGCTTGAACGATCTCTCAACTCTCCCGGCT 354
 DB 1425873 AAAACTGGAAGTCTGCCCCCTGAAACCGCTTGAACGATCTCTCAACTCTCCCGGCT 1425814
 QY 355 GAGACCTCTTGAGCGGAGAGACCCAGGCCCCAGAAAAACCCCTGAGCCCTGAGCCCTGAG 414
 DB 1425813 GAGACCTCTTGAGCGGAGAGACCCAGGCCCCAGAAAAACCCCTGAGCCCTGAGCCCTGAG 1425754
 QY 415 GTGACAACCGACCTCAAGAGAGACCACTAGACCAACCCCGGAAAGATACAGATTA 474
 DB 1425753 ATTAACAACCGACCTCAAGAGAGACCACTAGACCAACCCCGGAAAGATACAGATTA 1425694
 QY 475 TGAAGTCCCTCAGCCGCTCTGTTCCCAAGCATCTCCAGGACCAACCGCTCTCCACCC 534
 DB 1425693 TGAAGTCCCTCAGCCGCTCTGTTCCCAAGCATCTCCAGGACCAACCGCTCTCCACCC 1425634
 QY 535 TCTGATTCGCCGTAATCTTCCCAATTAGCTATCTCTTAAACCTCTTCAATTC 594
 DB 1425633 TCTGATTCGCCGTAATCTTCCCAATTAGCTATCTCTTAAACCTCTTCAATTC 1425574
 QY 595 CTCGGTTTATTCGAAACCGGTAAAGTGCTGTCTCAATATTCCTGCTCCCTGAGA 654
 DB 1425573 CTCGGTTTATTCGAAACCGGTAAAGTGCTGTCTCAATATTCCTGCTCCCTGAGA 1425514
 QY 655 TCCATCTTACTAGTCTCATATGCCCCGTTTTTCTCTGACAGCTTAAGCTACTCTCTA 714
 DB 1425513 TCCATCTTACTAGTCTCATATGCCCCGTTTTTCTCTGACAGCTTAAGCTACTCTCTA 1425454
 QY 715 CTCGCTCCAGAGCTCGGCCCCCACTACCTCCACCGGCTTCTGCGCGGAGATCG 774
 DB 1425453 CTCGCTCCAGAGCTCGGCCCCCACTACCTCCACCGGCTTCTGCGCGGAGATCG 1425394
 QY 775 CTGGGGCAGGCTATGCTACTGTGT 799
 DB 1425393 CTGGGGCAGGCTATGCTACTGTGT 834
 QY 835 ATCAGTAGACAGCTGCTCTTCCATGAAACGAAAAATCAATGTTTCTTAA 891
 DB 1425333 ATCAGTAGACAGCTGCTCTTCCATGAAACGAAAAATCAATGTTTCTTAA 1425277

RESULT 8

US-10-312-841-2
 ; Sequence 2, Application US/10312841
 ; Publication No. US20030186277A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Epigenomics AG
 ; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
 ; FILE REFERENCE: B01/1208/WO
 ; CURRENT APPLICATION NUMBER: US/10/312, 841
 ; CURRENT FILING DATE: 2002-12-30
 ; NUMBER OF SEQ ID NOS: 2
 ; SEQ ID NO 2
 ; LENGTH: 3673778
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence

FEATURE:
NAME/KEY: modified_base
LOCATION: (139)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (146)..(148)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (151)..(152)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (155)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (172)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (179)..(180)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (182)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (185)..(188)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (192)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (194)..(195)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (210)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (212)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (214)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (219)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (222)..(225)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (229)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (231)..(232)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (238)..(239)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:

NAME/KEY: modified_base
LOCATION: (242)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (245)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (248)..(260)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (265)..(270)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (272)..(276)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (278)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (282)..(283)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (287)..(290)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (302)..(306)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (311)..(313)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (323)..(334)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (336)..(341)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (345)..(363)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (365)..(368)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (370)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (374)..(375)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (379)..(385)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (387)..(388)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base

RESULT 11
US-10-292-798-1191/c
; Sequence 1191, Application US/10292798

```

1 Publication No.: US20030235833A1
2 GENERAL INFORMATION:
3 APPLICANT: SUMA, MAKIKO
4 APPLICANT: ASAI, KIYOSHI
5 APPLICANT: AKIYAMA, YUTAKA
6 APPLICANT: ABEURATANI, HIROYUKI
7 TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
8 FILE REFERENCE: 084335/166
9 CURRENT APPLICATION NUMBER: US/10/292,798
10 PRIOR FILING DATE: 2002-11-13
11 PRIOR FILING DATE: 2001-12-18
12 PRIOR APPLICATION NUMBER: JP 2001-246789
13 PRIOR FILING DATE: 2001-06-18
14 NUMBER OF SEQ ID NOS: 2070
15 SOFTWARE: PatentIn Ver. 2.1
16 SEQ ID NO 1191
17 LENGTH: 3133
18 TYPE: DNA
19 ORGANISM: Homo sapiens
20 FEATURE:
21 LOCATION: source
22 FEATURE:
23 LOCATION: (1)..(3133)
24 FEATURE:
25 NAME/KEY: CDS
26 LOCATION: (201)..(2933)
27 FEATURE:
28 NAME/KEY: modified base
29 LOCATION: (1)..(118)
30 OTHER INFORMATION: a, t, c, g, unknown or other
31 FEATURE:
32 NAME/KEY: modified base
33 LOCATION: (124)..(129)
34 OTHER INFORMATION: a, t, c, g, unknown or other
35 FEATURE:
36 NAME/KEY: modified base
37 LOCATION: (139)..(139)
38 OTHER INFORMATION: a, t, c, g, unknown or other
39 FEATURE:
40 NAME/KEY: modified base
41 LOCATION: (151)..(152)
42 OTHER INFORMATION: a, t, c, g, unknown or other
43 FEATURE:
44 NAME/KEY: modified base
45 LOCATION: (146)..(148)
46 OTHER INFORMATION: a, t, c, g, unknown or other
47 FEATURE:
48 NAME/KEY: modified base
49 LOCATION: (155)..(155)
50 OTHER INFORMATION: a, t, c, g, unknown or other
51 FEATURE:
52 NAME/KEY: modified base
53 LOCATION: (172)..(172)
54 OTHER INFORMATION: a, t, c, g, unknown or other
55 FEATURE:
56 NAME/KEY: modified base
57 LOCATION: (179)..(180)
58 OTHER INFORMATION: a, t, c, g, unknown or other
59 FEATURE:
60 NAME/KEY: modified base
61 LOCATION: (182)..(182)
62 OTHER INFORMATION: a, t, c, g, unknown or other
63 FEATURE:
64 NAME/KEY: modified base
65 LOCATION: (185)..(188)
66 OTHER INFORMATION: a, t, c, g, unknown or other
67 FEATURE:
68 NAME/KEY: modified base
69 LOCATION: (192)..(192)
70 OTHER INFORMATION: a, t, c, g, unknown or other
71 FEATURE:
72 NAME/KEY: modified base

```

DB	Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps	Matches
Db	312 CCCTGAACCGCGCTGAAGAGATCTCTCTCAACCTCTCCCGGCGCTGAACGACCTTGTGGCGGC	6.9%	61.8	15	313	0	0	0	744
Db	803 CC	3.4%	5.6	-08	744	413	0	0	744
Db	863 NCCC	0	0	0	804	0	0	0	804
Db	252 TCCTCGCGCTACCGCGCCGAGTGTCTCCCTGAGAGACCTGCTGAACCTGAGTCTGGCC	6.9%	61.8	15	313	0	0	0	744
Db	923 CCNCGN	3.4%	5.6	-08	744	413	0	0	744
Db	192 GCGTGAAGGCG	6.9%	61.8	15	313	0	0	0	744
Db	983 CCGTGAAGGCG	3.4%	5.6	-08	744	413	0	0	744
Db	132 CGAGGCG	6.9%	61.8	15	313	0	0	0	744
Db	983 CCGTGAAGGCG	3.4%	5.6	-08	744	413	0	0	744
Db	192 GCGTGAAGGCG	6.9%	61.8	15	313	0	0	0	744
Db	923 CCNCGN	3.4%	5.6	-08	744	413	0	0	744
Db	252 TCCTCGCGCTACCGCGCCGAGTGTCTCCCTGAGAGACCTGCTGAACCTGAGTCTGGCC	6.9%	61.8	15	313	0	0	0	744
Db	863 NCCC	0	0	0	804	0	0	0	804
Db	312 CCCTGAACCGCGCTGAAGAGATCTCTCTCAACCTCTCCCGGCGCTGAACGACCTTGTGGCGGC	6.9%	61.8	15	313	0	0	0	744
Db	803 CC	3.4%	5.6	-08	744	413	0	0	744

Dy 372 AGAGCCCCAGGCCCCAGAAAAACCCCTGGCCTCTGTGCCTTAGGTGGACAACCGACTCA 437
Dy 743 NCCCCCNCCCNNNNNCCNNNCCCCCCCCCCCCCNCNCNCCCCCNCCCCCCCCCCC 684
Dy 432 GAGAGACCAGACTTGAACCCAGGGAGAAGTAAGATATATGATGCCCTCAGCG 491
Dy 683 CCNNNNCCCCCCCCNNCCCCCCCCCCCCCNCNNNNCCCCCCCCCCCCCCCCCCCC 624
Dy 492 TTCTGTTTCCAGGCAITCCAGGCAACGACCTCTCCACCTCTGAATTCCCGTAAT 551
Dy 623 CANNCCNCCCCCCCCCCCCNNCCNNCCNNCCCCCCCCCCCCNNCCNNCCNN 564
Dy 552 TCTTCCCAATTGAGCTATCTCTTAAACCTCTTCTCATTCCTCGGTTTTATTCTGAA 611
Dy 563 CCCCCCCCCCNNNNCCCCCNCNCCCCCCCCCNNNNCCCCCCCCCCCC 504
Dy 612 CCGTAGGTGTGTCTCATATTTCTGTCCCTCCGAGATGCATACTTGATGCTCA 671
Dy 503 CCNCCNCCNNNNCCCCNCCNCCNCCCCCCCCCCCCCNCNCCNCCNCCNNCCNN 444
Dy 672 CATGCCCGTTTTTCTCTGAAGAAGCTACTCTCTACCTGACTCCAGGCTC 731
Dy 443 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCNCNCCNCCNCCNNCCNNCCN 384
Dy 732 GGCCCACTCACTCCACG 751
Dy 383 NNNNNCCNNCCNNNNNC 364

LOCATION: (199)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (214)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (218)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (221)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (229)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (232)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (235) ..(236)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (246)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (248) ..(252)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (256) ..(257)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (261) ..(263)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (265) ..(266)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (271) ..(273)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (283) ..(285)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (296)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (298) ..(300)	
OTHER INFORMATION: a, t, c, g, unknown or other	
FEATURE:	
NAME/KEY: modified_base	
LOCATION: (302)	

```
Db 4672 CCCCCCCCCCNCCNNCCCCCCCCCCCCCNCCNNCCNNNTTTTCCCCCCCCCCC 4613
QY 321 GCCTAGAACGATCTCTCTCAACTCCCGGCTGAGACCTTGGCCGAGAGACCCA 380
Db 4612 NNNCCCCCCCCCCCCCNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCC 4553
QY 381 GCCCCAGAAACCCCTGGCCCTCTGGCCCTGAGGTGAGCAACCGACTCAGAGAGAGCC 440
Db 4552 CNNCCNNNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCC 4493
QY 441 AGACTTAGACCCACCCCGGAGAGTACAGATAATGAGATCCCTCAGCCGTTCTGTTCC 500
Db 4492 CCCCCCCCCCCCCCNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCC 4433
QY 501 CAGGCACTTCAGAGCAGCAGAGCCCTCTCAGACCTCTGATTCCTGATTCCTGAA 560
Db 4432 NNNNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCC 4373
QY 561 TTAGCTATCTCTTAACCTCTTCTCAATTCCTCGGTTTATCTGAACCGTAAG 620
Db 4372 NNNNNNNNNNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCC 4313
QY 621 TGGTGTCTCAATATTTCTGTCCCTCTGAGATTCATACTTAGTCTCAATGCGCG 680
Db 4312 CCNCCCCCCCCCNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCC 4253
QY 681 TTTTCTCTGACAGCTTAAGCTACTCTCTACTCTGCTCTCAGGCTCGGCCCCACC 740
Db 4252 CCCCCCCCNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCC 4193
QY 741 TACCTCCACCGGCTTCTCTGCGCG 767
Db 4192 NNNNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCC 4166
```

Search completed: January 11, 2005, 09:25:14
Job time : 609 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 11, 2005, 06:07:34 ; Search time 540 Seconds
(without alignments)
8661.545 Million cell updates/sec

Title: US-09-994-365-1
Perfect score: 891
Sequence: 1 ccctctggggtccacagca.....taaaatcatgttctttaa 891

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	891	100.0	891	6	ABK86962 Human can
2	886.2	99.5	1473	6	ABN60006 Novel hum
3	775.4	87.0	2997	6	ABK86967 Human CAN
4	775.4	87.0	3001	6	ABK86963 Human can
5	775	87.0	55050	4	ABQ75680 Human SER
6	773.8	86.8	25235	4	AAH45310 Human SER
7	563.4	63.2	565	12	ACH72505 Human gen
8	157	17.6	157	12	ACH86315 Human gen
9	61.8	6.9	3133	10	ADCH6738 Human gen
10	60	6.7	60	6	ABN32329 Human spl
11	55	6.2	1337	2	AAZ17263 Human gen
12	53	5.9	1218	3	AAZ17263 Human gen
13	52.8	5.9	5452	10	ADCH6736 Human GPC
14	51.8	5.8	12733	6	ABK96631 Vector pr
15	51.8	5.8	12733	6	ABK96631 Vector pr
16	51.8	5.8	12733	6	ABK96631 Vector pr
17	51.8	5.8	12733	6	ABK96631 Vector pr
18	50.4	5.7	3163	10	ADCH6736 Human GPC
19	50	5.6	50	6	ABZ00541 Human leu
20	48.8	5.5	1359	2	AAZ17254 Human gen
21	48.4	5.4	1833	4	ABL22159 Drosophila

C	22	48.2	5.4	1000	3	AAA02484	AA02484 Human col
C	23	47	5.3	1064	6	ABT09678	ABT09678 Human PAL
C	24	46.6	5.2	1117	10	ADCH6668	ADCH6668 Human GPC
C	25	46.2	5.2	10732	3	AAA10594	AA10594 Gene enco
C	26	45.4	5.1	1436	2	AAI5853	AA5853 Streptom
C	27	44.8	5.0	1327	6	ABQ68452	ABQ68452 Listeria
C	28	44.8	5.0	53522	2	AAAD30228	AA30228 Human PKD
C	29	44.8	5.0	53526	2	AAAT94101	AA94101 Human PKD
C	30	44.8	5.0	53577	2	AAAT8551	AA8551 Human pol
C	31	44.8	5.0	53577	2	AAAT94106	AA94106 Human PKD
C	32	44.2	5.0	536	6	ABQ36994	ABQ36994 Oligonuc
C	33	44.2	5.0	556	6	ABQ36995	ABQ36995 Oligonuc
C	34	44.2	5.0	1050	4	AAAD1685	AA1685 Mutaciona
C	35	44.2	5.0	2849	4	AAAD1684	AA1684 Human ret
C	36	43.6	4.9	1384	10	ADCH7450	ADCH7450 Human GPC
C	37	43	4.8	1459	3	AAA02528	AA02528 Human col
C	38	42.8	4.8	2000	8	ADAT1938	ADAT1938 Rice gene
C	39	42.6	4.8	799	2	AAV55831	AAV55831 Nucleotid
C	40	42.6	4.8	1926	3	AAA50254	AA50254 Epstein B
C	41	42.6	4.8	1926	4	AAAF2902	AAF2902 EBV lathe
C	42	42.6	4.8	1926	10	ADK65580	ADK65580 Human her
C	43	42.6	4.8	2580	3	AAAT75454	AA75454 Nucleotid
C	44	42.6	4.8	2580	6	AAAT64275	AA64275 Epstein-B
C	45	42.6	4.8	3198	2	AAAX02974	AA02974 Human IL-

ALIGNMENTS

RESULT 1	ABK86962	standard; cDNA; 891 BP.
ID	ABK86962	standard; cDNA; 891 BP.
XX	ABK86962;	
AC	ABK86962;	
XX	24-SEP-2002	(first entry)
DT	24-SEP-2002	(first entry)
XX	Human candidate coding sequence-1 (CAN-1) cDNA.	
DE	Human candidate coding sequence-1 (CAN-1) cDNA.	
XX	Human; antipeptidic; chromosome 6; candidate coding sequence-1; CAN-1;	
KW	SEK-1; STG; human leukocyte antigen C; HLA C; HLA Cw6; psoriasis; skin;	
KW	keratinocyte; chronic inflammatory dermatosis; erythroderma; seboreic;	
KW	gutrate; pustular variant; Reiter's disease; hyperproliferation;	
KW	epidermis; differentiation; diagnosis; gene therapy; gene; ss; SNP;	
KW	single nucleotide polymorphism.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	Location/Qualifiers	
XX	Key	64..474
XX	CDS	64..474
FT	sig_peptide	/product= "CAN-1"
FT	mat_peptide	/tag= b
FT	variation	/tag= c
FT	variation	/note= "Mature CAN-1"
FT	variation	/tag= d
FT	variation	/standard_name= "Single nucleotide polymorphism"
XX	W0200244375-A2.	
XX	06-JUN-2002.	
XX	27-NOV-2001; 2001WO-US044506.	
XX	28-NOV-2000; 2000US-0253592P	
XX	15-DEC-2000; 2000US-0256639P.	
XX	(CELL-) CELLTECH R & D INC.	
XX	Charmley P, Moss P, Mceuen M;	
XX	PI	

XX MPI; 2002-508513/54.
 DR P-PSDB; AAU9579.
 XX
 PT Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation
 PT and differentiation, and polynucleotides encoding the polypeptide, useful
 PT for diagnosing or predicting susceptibility to psoriasis in individual.
 XX
 PS Claim 8; Page 80-81; 95pp; English.

XX The invention discloses isolated candidate coding sequence-1 (CAN-1),
 CC SEBK-1 (not defined) and STG (not defined) polypeptides, and the
 CC polynucleotides encoding them. All three genes were identified due to
 CC their proximity to the human leukocyte antigen C (HLA C) locus on
 CC chromosome 6. The HLA Cw6 allele is associated with psoriasis and as the
 CC three genes are expressed in normal skin and/or keratinocyte tissue, they
 CC may also have a role in psoriasis. Psoriasis is a chronic inflammatory
 CC dermatosis that is characterized by hyperproliferation of epidermal
 CC cells. Possible treatments against psoriasis involve the inhibition of
 CC movement of cells into the epidermis, or the inhibition of
 CC hyperproliferation or abnormal differentiation of keratinocytes, by the
 CC inhibition of the CAN-1, STG or SEBK-1 polypeptides binding to their
 CC binding partners. The polypeptides are useful for diagnosing or
 CC predicting the susceptibility to psoriasis in an individual, for
 CC ameliorating the symptoms and/or progression of psoriasis and for
 CC identifying agents useful for treating psoriasis or modulating the
 CC activity of the polypeptide. The polypeptides are also useful for
 CC enhancing the level of CAN-1, STG or SEBK-1 biological activity in a cell
 CC or tissue. The nucleic acid molecules are useful as hybridisation probes
 CC in diagnostic procedures (such as diagnosing the presence of psoriasis or
 CC the propensity to develop psoriasis) and for suppressing the expression
 CC of CAN-1 or STG gene (e.g. antisense inhibition, gene therapy).
 CC Antibodies, raised against the polypeptides, are useful for decreasing
 CC the level of CAN-1, STG or SEBK-1 biological activity in a cell. The
 CC sequence presented is the human candidate coding sequence-1 (CAN-1) cDNA
 SQ Sequence 891 BP; 169 A; 339 C; 196 G; 187 T; 0 U; 0 Other;

Query Match 100.0%; Score 891; DB 6; Length 891;
 Best Local Similarity 100.0%; Pred. No. 3.9e-225;
 Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTGGGGGTTCCAGGACCCAGACTCCAGCCCACTTTGGGGGCCAGTACATA 60
 Db 1 CCTCTGGGGGTTCCAGGACCCAGACTCCAGCCCACTTTGGGGGCCAGTACATA 60
 QY 61 GCCATGATCTCTCAACTGGAAGCTCTGGGGATCTGTCTTTGCTGCAACAGAGGC 120
 Db 61 GCCATGATCTCTCAACTGGAAGCTCTGGGGATCTGTCTTTGCTGCAACAGAGGC 120
 QY 121 ATCTCAGGACGAGGAGGAGCCCTCTCACCACCCGAGAGAGAGAGAGGAGGC 180
 Db 121 ATCTCAGGACGAGGAGGAGCCCTCTCACCACCCGAGAGAGAGAGAGGAGGC 180
 QY 181 TCCCAACATTTGCTCAGGGCCCCCAGTCCCGGATGACCTTGGCAGGGGAGCCCT 240
 Db 181 TCCCAACATTTGCTCAGGGCCCCCAGTCCCGGATGACCTTGGCAGGGGAGCCCT 240
 QY 241 CTCTTTGAAGATCTCTCGCTACCCGCGAGTGTCTCTGAGAGAGACTGCTGAAACT 300
 Db 241 CTCTTTGAAGATCTCTCGCTACCCGCGAGTGTCTCTGAGAGAGACTGCTGAAACT 300
 QY 301 GAGTCTGGCCCCCTGAAACCGGCTAGAGAGGATCTCTCAACTCCCGGGCTGACGAC 360
 Db 301 GAGTCTGGCCCCCTGAAACCGGCTAGAGAGGATCTCTCAACTCCCGGGCTGACGAC 360
 QY 361 CTTTGGCCGAGAGACCCAGACCCCAAGAAACCTTGAGCTCTGCTCCCTTAAGTGGAC 420
 Db 361 CTTTGGCCGAGAGACCCAGACCCCAAGAAACCTTGAGCTCTGCTCCCTTAAGTGGAC 420
 QY 421 AACCGACCTCAGT 480
 Db 421 AACCGACCTCAGT 480

QY 481 CCCCTACGCCGTTCTGTTCACAGACATCTCCAGGACCCAGCCCTCTCCACCTCTGAT 540
 Db 481 CCCCTACGCCGTTCTGTTCACAGGACATCTCCAGGACCCAGCCCTCTCCACCTCTGAT 540
 QY 541 TCCCGGAGATCTCTCCCAATTTAGGCTATCTCTTAAACCTTCTCTGATTCCTGGGT 600
 Db 541 TCCCGGAGATCTCTCCCAATTTAGGCTATCTCTTAAACCTTCTCTGATTCCTGGGT 600
 QY 601 TTATTTGAAACCCGTAAGGTGTGTCTCAATATTTCCGTCCCTCCGAGATCCATA 660
 Db 601 TTATTTGAAACCCGTAAGGTGTGTCTCAATATTTCCGTCCCTCCGAGATCCATA 660
 QY 661 CTTAGTCTCAATTCGCCGCTTTTCTCTCTGACAGCTTAAGCTTACTCTACCTGCG 720
 Db 661 CTTAGTCTCAATTCGCCGCTTTTCTCTCTGACAGCTTAAGCTTACTCTACCTGCG 720
 QY 721 CTCAGGACCTCGAGCCCACTACCTCCACCCGGTCTCTGCGCGGAGATCGCTGGG 780
 Db 721 CTCAGGACCTCGAGCCCACTACCTCCACCCGGTCTCTGCGCGGAGATCGCTGGG 780
 QY 781 CAGGCTATGTAATGTGTTCCTTCTCTGCACTGAGCGGCGAGAACTATCAAT 840
 Db 781 CAGGCTATGTAATGTGTTCCTTCTCTGCACTGAGCGGCGAGAACTATCAAT 840
 QY 841 AGACAGCTGCTGCTTCATGAAACGGAATAAATCAATGTTTCTTAA 891
 Db 841 AGACAGCTGCTGCTTCATGAAACGGAATAAATCAATGTTTCTTAA 891

RESULT 2
 ABN60006
 ID ABN60006 standard; cDNA; 1473 BP.
 XX

AC ABN60006;

DT 28-JUN-2002 (first entry)

DE Novel human coding sequence SEQ ID NO: 417.

KW Human; antianemic; vulnery; antiinflammatory; immunomodulator;
 KW antifertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
 KW neuroprotective; antiparkinsonian; protein therapy; EST;
 KW expressed sequence tag; gene; ss.

OS Homo sapiens.

PN WO200222660-A2.

PD 21-MAR-2002.

PF 10-SEP-2001; 2001WO-US026015.

PR 11-SEP-2000; 2000US-00659671.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;

DR MPI; 2002-292408/33.
 DR P-PSDB; ABB97593.

XX An isolated polynucleotide for treating diseases associated with its
 PT encoded polypeptide such as cancer and multiple sclerosis.
 XX

PS Claim 1; SEQ ID NO 417; 509pp; English.

CC The present invention provides the protein and coding sequences of 444
 CC novel human proteins. These were isolated from expressed sequences tags
 CC (ESTs). They can be used to stimulate cell growth, to regulate
 CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
 CC e.g. in burn treatment, to regulate the immune system e.g. to treat

CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC infertility, to regulate haemostasis e.g. to treat stroke
CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.
CC rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a coding sequence of the
CC invention

XX Sequence 1473 BP; 294 A; 491 C; 382 G; 306 T; 0 U; 0 Other;

Query Match 99.5%; Score 886.2; DB 6; Length 1473;
Best Local Similarity 99.7%; Pred. No. 8.7e-224;
Matches 888; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCTCTGGGGTTCCTCAGGACCCAGACTCAGCCACCCAGCTTTGGGGGCACTACATA 60
DB 573 CCTCTGGGGTTCCTCAGGACCCAGACTCAGCCACCCAGCTTTGGGGGCACTACATA 632
QY 61 GCCATGATCTCACTGAAAGCTCTGGGATCTGTGCTTTGCTGCAACCCAGAGGC 120
DB 633 GCCATGATCTCACTGAAAGCTCTGGGATCTGTGCTTTGCTGCAACCCAGAGGC 692
QY 121 ATCTCAGGACGAGGGGCACTCTTCACTCCAGGACCGAGAGAGGAGGAGGC 180
DB 693 ATCTCAGGACGAGGGGCACTCTTCACTCCAGGACCGAGAGAGGAGGAGGC 752
QY 181 TCCCAACATTTGCTCAGGGGCCCCCAGTCCCGGATGACCTTGGGAGGAGGAGGC 240
DB 753 TCCCAACATTTGCTCAGGGGCCCCCAGTCCCGGATGACCTTGGGAGGAGGAGGC 812
QY 241 CTCTTTGAAAGTCTTCCGCTTACCCGCCCCAGTGTCTCTGAGAGAGACTGCTGAAACT 300
DB 813 CTCTTTGAAAGTCTTCCGCTTACCCGCCCCAGTGTCTCTGAGAGAGACTGCTGAAACT 872
QY 301 GGAATCTGGGCCCCCTGAAACCGCTGAAAGGATCTCTCTCACTCCCGGCTGAGAGAC 360
DB 873 GGAATCTGGGCCCCCTGAAACCGCTGAAAGGATCTCTCTCACTCCCGGCTGAGAGAC 932
QY 361 CCTTGGCGGAGAGACCCAGGCCCCCAAGAAAACCTGGGCTCTGGCCCCCTGAGAGGAGAC 420
DB 933 CCTTGGCGGAGAGACCCAGGCCCCCAAGAAAACCTGGGCTCTGGCCCCCTGAGAGGAGAC 992
QY 421 AACGCACTCAG 480
DB 993 AACGCACTCAG 1052
QY 481 CCCCCTCAGCGGTTGTGTTCCAGGATCTCAGGAGACCCAGGCTCTCCACCTCTGAT 540
DB 1053 CCCCCTCAGCGGTTGTGTTCCAGGATCTCAGGAGACCCAGGCTCTCCACCTCTGAT 1112
QY 541 TCCCGGAGAAATCTTCCCAATTTAGGCTATCTCTTAAACCTCTTCCATTCCTGGGT 600
DB 1113 TCCCGGAGAAATCTTCCCAATTTAGGCTATCTCTTAAACCTCTTCCATTCCTGGGT 1172
QY 601 TTTATTTGAAACCGGTAAGGTGTGTTCTCAATATTTTCTGTGCTCCCTCTGAGATCCATA 660
DB 1173 TTTATTTGAAACCGGTAAGGTGTGTTCTCAATATTTTCTGTGCTCCCTCTGAGATCCATA 1232
QY 661 CTTAGTCTCAATGCGCCGTTTTTCTCTGACAGCTTAAGCTTCTCTACCTGGC 720
DB 1233 CTTAGTCTCAATGCGCCGTTTTTCTCTGACAGCTTAAGCTTCTCTACCTGGC 1292
QY 721 CTCGAGGCTCGGGCCAGCACTCCGAGCCGCTTCCGAGCCGGGAGATGGCTGGGG 780
DB 1293 CTCGAGGCTCGGGCCAGCACTCCGAGCCGCTTCCGAGCCGGGAGATGGCTGGGG 1352
QY 781 CAGGGCTATGATGTGTTCCCTTCTGCACTGTGTGCGGCGGAGAGAACTATCAGT 840
DB 1353 CAGGGCTATGATGTGTTCCCTTCTGCACTGTGTGCGGCGGAGAGAACTATCAGT 1412
QY 841 AGACAGCTGCTGCTTCCATGAAACGGAATAATTAATCATGTTTCTTAA 891
DB 1413 AGACAGCTGCTGCTTCCATGAAACGGAATAATTAATCATGTTTCTTAA 1463

RESULT 3
ID ABR66967 standard; DNA; 2997 BP.
XX ABR66967;
AC
XX
XX
XX 24-SEP-2002 (first entry)
DB Human CAN-1 deletion polymorphism genomic DNA.
XX
XX Human; antipsoriatic; chromosome 6; candidate coding sequence-1; CAN-1;
XX SEER-1; STG; human leukocyte antigen C; HLA C; HLA Cw6; psoriasis; skin;
XX keratinocyte; chronic inflammatory dermatosis; erythroderma; seboreic;
XX guttate; pustular variant; Reiter's disease; hyperproliferation;
XX epidermis; differentiation; diagnosis; gene therapy; gene; ds; SNP;
XX Single nucleotide polymorphism; deletion polymorphism.
OS
XX
XX Homo sapiens.
FH Key
FT variation
FT Location/Qualifiers
FT /tag= a
FT /note= "Deletion polymorphism"
FT replace(114,T)
FT /tag= b
FT /standard name= "Single nucleotide polymorphism"
FT replace(361,A)
FT /tag= c
FT /standard name= "Single nucleotide polymorphism"
FT replace(550,A)
FT /tag= d
FT /standard name= "Single nucleotide polymorphism"
FT replace(966,G)
FT /tag= e
FT /standard name= "Single nucleotide polymorphism"
FT replace(1096,T)
FT /tag= f
FT /standard name= "Single nucleotide polymorphism"
FT replace(1196,A)
FT /tag= g
FT /standard name= "Single nucleotide polymorphism"
FT replace(1390,T)
FT /tag= h
FT /standard name= "Single nucleotide polymorphism"
FT 1461..2557
FT /tag= i
FT /product= "CAN-1"
FT 1481..1535
FT /tag= j
FT /number= 1
FT 1536..2201
FT /tag= k
FT /number= 1
FT /tag= l
FT /number= 1
FT /tag= m
FT /standard name= "Single nucleotide polymorphism"
FT replace(1875,T)
FT /tag= n
FT /standard name= "Single nucleotide polymorphism"
FT replace(1982,A)
FT /tag= o
FT /standard name= "Single nucleotide polymorphism"
FT replace(2016,C)
FT /tag= p
FT /standard name= "Single nucleotide polymorphism"
FT replace(2107,G)
FT /tag= q
FT /standard name= "Single nucleotide polymorphism"
FT 2202..2257
FT /tag= r
FT /number= 2
FT replace(2393,T)
FT variation

```
FT      /tag= r
FT      /standard_name= "Single nucleotide polymorphism"
FT      /replace(2551,G)
FT      /*tag= s
FT      /standard_name= "Single nucleotide polymorphism"
FT      /replace(2818,G)
FT      /*tag= t
FT      /standard_name= "Single nucleotide polymorphism"
FT      /replace(2871,C)
FT      /*tag= u
FT      /standard_name= "Single nucleotide polymorphism"
XX      MO200244375-A2.
XX      06-JUN-2002.
XX      27-NOV-2001; 2001WO-US044506.
XX      28-NOV-2000; 2000US-0253592P.
XX      15-DEC-2000; 2000US-0256839P.
XX      (CELL-) CELTECH R & D INC.
XX      Charnley P, Moss P, Mceuen M;
XX      WPI; 2002-508513/54.
XX      P-PSDB; AAU79579.
XX      Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation
XX      and differentiation, and polynucleotides encoding the polypeptide; useful
XX      for diagnosing or predicting susceptibility to psoriasis in individual.
XX      Example 3; Page 92-93; 95pp; English.
XX      The invention discloses isolated candidate coding sequence-1 (CAN-1),
XX      SEEK-1 (not defined) and STG (not defined) polypeptides, and the
XX      polynucleotides encoding them. All three genes were identified due to
XX      their proximity to the human leukocyte antigen C (HLA C) locus on
XX      chromosome 6. The HLA Cw6 allele is associated with psoriasis and as the
XX      three genes are expressed in normal skin and/or keratinocyte tissue, they
XX      may also have a role in psoriasis. Psoriasis is a chronic inflammatory
XX      dermatosis that is characterised by hyperproliferation of epidermal
XX      cells. Possible treatments against psoriasis involve the inhibition of
XX      movement of cells into the epidermis, or the inhibition of
XX      hyperproliferation or abnormal differentiation of keratinocytes, by the
XX      inhibition of the CAN-1, STG or SEEK-1 polypeptides binding to their
XX      binding partners. The polypeptides are useful for diagnosing or
XX      predicting the susceptibility to psoriasis in an individual, for
XX      ameliorating the symptoms and/or progression of psoriasis and for
XX      identifying agents useful for treating psoriasis or modulating the
XX      activity of the polypeptide. The polypeptides are also useful for
XX      enhancing the level of CAN-1, STG or SEEK-1 biological activity in a cell
XX      or tissue. The nucleic acid molecules are useful as hybridisation probes
XX      in diagnostic procedures (such as diagnosing the presence of psoriasis or
XX      the propensity to develop psoriasis) and for suppressing the expression
XX      of CAN-1 or STG gene (e.g. antisense inhibition, gene therapy).
XX      Antibodies, raised against the polypeptides, are useful for decreasing
XX      the level of CAN-1, STG or SEEK-1 biological activity in a cell. The
XX      sequence presented is the human candidate coding sequence-1 (CAN-1)
XX      deletion polymorphism genomic DNA
XX      Sequence 2997 BP; 617 A; 785 C; 913 G; 682 T; 0 U; 0 Other;
SQ      Query Match      87.0%; Score 775.4; DB 6; Length 2997;
      Best Local Similarity 99.9%; Pred. No. 2,1e-194;
      Matches 776; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      115 AGAGGACATCTCAGGACGAGGCGCACCTCTTCCACCCACCGCAGAGAGAGAG 174
DB      2198 ACAGGACATCTCAGGACGAGGCGCACCTCTTCCACCCACCGCAGAGAGAG 2257
QY      175 GCAGGCTCCCGACATTTGCTCAGGGGCCCCCGCATGCCGCTACCTTGGCCAGGGGCA 234
```

```
DB      2258 GCAGGCTCCCGACATTTGCTCAGGGGCCCCCGCATGCCGCTACCTTGGCCAGGGGCA 2317
QY      235 CCCCCTCTCTTTAAGATTCCTCCGCTACCGCGCCAGTGCTCTGGAGAGACTGCTT 294
DB      2318 CCCCCTCTCTTTAAGATTCCTCCGCTACCGCGCCAGTGCTCTGGAGAGACTGCTT 2377
QY      295 GAAACTGAGATCTGGGCCCCCTGAGACCGCTTGAACGAGATCTCTTCAACTCTCCCGGCT 354
DB      2378 GAAACTGAGATCTGGGCCCCCTGAGACCGCTTGAACGAGATCTCTTCAACTCTCCCGGCT 2437
QY      355 GAGACCCCTTTGGCGCGGAGACCCCGACCCCGCGAGAAAACCTTGGCTCTCTGCCCCCTGAG 414
DB      2438 GAGACCCCTTTGGCGCGGAGACCCCGACCCCGCGAGAAAACCTTGGCTCTCTGCCCCCTGAG 2497
QY      415 GTGAGCAACCGACCTCAGAGAGAGACCGACCTAGACCCACCCCGGAGAGAGTACAGATTA 474
DB      2498 GTGAGCAACCGACCTCAGAGAGAGACCGACCTAGACCCACCCCGGAGAGAGTACAGATTA 2557
QY      475 TGAAGTCCCTCAGCCGCTGCTTCCAGGACATCTCAGGACCAACGCGCTCTCCACCC 534
DB      2558 TGAAGTCCCTCAGCCGCTGCTTCCAGGACATCTCAGGACCAACGCGCTCTCCACCC 2617
QY      535 TCTGATTTCCCGGTGATTTCTTCCCAATTTAGCTTATCTCTTAAACCTCTTCTCATTTCC 594
DB      2618 TCTGATTTCCCGGTGATTTCTTCCCAATTTAGCTTATCTCTTAAACCTCTTCTCATTTCC 2677
QY      595 CTCGGTTTATTTGTAACCCGTAAAGGTGATGTTCTCAATATTTCTGTCGCCCTCTGAGA 654
DB      2678 CTCGGTTTATTTGTAACCCGTAAAGGTGATGTTCTCAATATTTCTGTCGCCCTCTGAGA 2737
QY      655 TCCATATTAATGTCATCATGCGCGGTTTTTCTCTGACAGCTTAAAGCTACTCTCTTA 714
DB      2738 TCCATATTAATGTCATCATGCGCGGTTTTTCTCTGACAGCTTAAAGCTACTCTCTTA 2797
QY      715 CCTGGCTCTCAGGACCTCCGCGCCCACTACTCTCCACCGCGTCTTCTGCCCCGCGATG 774
DB      2798 CCTGGCTCTCAGGACCTCCGCGCCCACTACTCTCCACCGCGTCTTCTGCCCCGCGATG 2857
QY      775 CTCGGGCAAGGCTATGATGATGTTCCCTTCTGCACTGTGAGCGCGGAGAGAACT 834
DB      2858 CTCGGGCAAGGCTATGATGATGTTCCCTTCTGCACTGTGAGCGCGGAGAGAACT 2917
QY      835 ATCAGTAGACAGCTGCTCTTCCATGAACGAAAAATTAATCATGTTTCTTAA 891
DB      2918 ATCAGTAGACAGCTGCTCTTCCATGAACGAAAAATTAATCATGTTTCTTAA 2974
RESULT 4
ABK86963
ID      ABK86963 standard; DNA; 3001 BP.
XX      ABK86963;
AC      24-SEP-2002 (first entry)
XX      DT
XX      DE
XX      Human candidate coding sequence-1 (CAN-1) genomic DNA.
XX      DE
XX      Human; antipsoriatic; chromosome 6; candidate coding sequence-1; CAN-1;
XX      SEEK-1; STG; human leukocyte antigen C; HLA C; HLA Cw6; psoriasis; skin;
XX      keratinocyte; chronic inflammatory dermatosis; erythroderma; seborethic;
XX      guttate; pustular variant; Reiter's disease; hyperproliferation;
XX      epidermis; differentiation; diagnosis; gene therapy; gene; de; SNP;
XX      single nucleotide polymorphism; deletion polymorphism.
OS      Homo sapiens.
FH      Key
FH      Location/Qualifiers
FT      variation
FT      /*tag= a
FT      /note= "Deletion polymorphism"
FT      /replace(118,T)
FT      /*tag= b
FT      /standard_name= "Single nucleotide polymorphism"
```



```
FT variation replace(554,A)
FT /*tag= c
FT /standard_name= "Single nucleotide polymorphism"
FT replace(1100,T)
FT /*tag= d
FT /standard_name= "Single nucleotide polymorphism"
FT replace(1500,A)
FT /*tag= e
FT /standard_name= "Single nucleotide polymorphism"
FT replace(1594,T)
FT /*tag= f
FT /standard_name= "Single nucleotide polymorphism"
FT CDS 1485..2561
FT /*product= "CAN-1"
FT 1485..1539
FT /*tag= h
FT /number= 1
FT 1540..2205
FT /*tag= i
FT /number= 1
FT intron replace(1661,A)
FT /*tag= j
FT /standard_name= "Single nucleotide polymorphism"
FT replace(1879,T)
FT /*tag= k
FT /standard_name= "Single nucleotide polymorphism"
FT replace(1986,A)
FT /*tag= l
FT /standard_name= "Single nucleotide polymorphism"
FT replace(2020,C)
FT /*tag= m
FT /standard_name= "Single nucleotide polymorphism"
FT replace(2111,G)
FT /*tag= n
FT /standard_name= "Single nucleotide polymorphism"
FT 2206..2561
FT /*tag= o
FT /number= 2
FT replace(2397,T)
FT /*tag= p
FT /standard_name= "Single nucleotide polymorphism"
FT replace(2655,G)
FT /*tag= q
FT /standard_name= "Single nucleotide polymorphism"
FT replace(2822,G)
FT /*tag= r
FT /standard_name= "Single nucleotide polymorphism"
FT replace(2875,C)
FT /*tag= s
FT /standard_name= "Single nucleotide polymorphism"
FT MO200244375-A2.
FT PN
FT PD 06-JUN-2002.
FT XX
FT PF 27-NOV-2001; 2001WO-US044506.
FT XX
FT PR 28-NOV-2000; 2000US-0253592P.
FT PR 15-DEC-2000; 2000US-0256839P.
FT XX
FT PA (CELL-) CELLTECH R & D INC.
FT PI Charmley P, Mosa P, Mceuen M;
FT XX WPI; 2002-508513/54.
FT DR P-PSDB; AAU79579.
FT XX
FT Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation
FT and differentiation, and polynucleotides encoding the polypeptide, useful
FT for diagnosing or predicting susceptibility to psoriasis in individual.
FT PS Claim 18; Page 82-84; 95pp; English.
```

```
XX The invention discloses isolated candidate coding sequence-1 (CAN-1),
CC SEBK-1 (not defined) and STG (not defined) polypeptides, and the
CC polynucleotides encoding them. All three genes were identified due to
CC their proximity to the human leukocyte antigen C (HLA C) locus on
CC chromosome 6. The HLA Cw6 allele is associated with psoriasis and as the
CC three genes are expressed in normal skin and/or keratinocyte tissue, they
CC may also have a role in psoriasis. Psoriasis is a chronic inflammatory
CC dermatosis that is characterized by hyperproliferation of epidermal
CC cells. Possible treatments against psoriasis involve the inhibition of
CC movement of cells into the epidermis, or the inhibition of
CC hyperproliferation or abnormal differentiation of keratinocytes, by the
CC inhibition of the CAN-1, STG or SEBK-1 polypeptides binding to their
CC binding partners. The polypeptides are useful for diagnosing or
CC predicting the susceptibility to psoriasis in an individual, for
CC ameliorating the symptoms and/or progression of psoriasis and for
CC identifying agents useful for treating psoriasis or modulating the
CC activity of the polypeptide. The polypeptides are also useful for
CC enhancing the level of CAN-1, STG or SEBK-1 biological activity in a cell
CC or tissue. The nucleic acid molecules are useful as hybridisation probes
CC in diagnostic procedures (such as diagnosing the presence of psoriasis or
CC the propensity to develop psoriasis) and for suppressing the expression
CC of CAN-1 or STG gene (e.g. antisense inhibition, gene therapy).
CC Antibodies, raised against the polypeptides, are useful for decreasing
CC the level of CAN-1, STG or SEBK-1 biological activity in a cell. The
CC sequence presented is the human candidate coding sequence-1 (CAN-1)
CC genomic DNA
CC
XX
SQ Sequence 3001 BP; 619 A; 786 C; 914 G; 682 T; 0 U; 0 Other;
Query Match 87.0%; Score 775.4; DB 6; Length 3001;
Best Local Similarity 99.9%; Pred. No. 2,1e-194;
Matches 776; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 115 AGAGGATCTCAGGACGAGGAGGACCCCTCTCAACCCGACGAGGAGGAG 174
DB 2202 ACAGGATCTCAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2261
QY 175 GAGAGTCCCAATGCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 234
DB 2262 GAGAGTCCCAATGCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2321
QY 235 CCCCCTCTTTGAAGATCTCCGCTACCCGAGGAGGAGGAGGAGGAGGAGGAG 294
DB 2322 CCCCCTCTTTGAAGATCTCCGCTACCCGAGGAGGAGGAGGAGGAGGAGGAG 2381
QY 295 GAAACTGAGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 354
DB 2382 GAAACTGAGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2441
QY 355 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 414
DB 2442 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2501
QY 415 GTGAGCAACGAGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 474
DB 2502 GTGAGCAACGAGCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2561
QY 475 TGAAGTCCCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 534
DB 2562 TGAAGTCCCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2621
QY 535 TGTGATTCCTCCGAGATCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 594
DB 2622 TGTGATTCCTCCGAGATCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2681
QY 595 CTGGTTTATTTGAACCCGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 654
DB 2682 CTGGTTTATTTGAACCCGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2741
QY 655 TCATATTAGTCTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 714
DB 2742 TCATATTAGTCTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2801
```

QY 715 CCTGCGCTCCAGGCGCTGCGCCCACTACCTCCAGCCGCTTCTGCGCGCGGATCG 774
 DB 2802 CCTGCGCTCCAGGCGCTGCGCCCACTACCTCCAGCCGCTTCTGCGCGCGGATCG 2861
 QY 775 CTGCGGCGAGGCGCTATGTAAGTGTGTTCCCTTCTGCGCACTGAGCGCGCGAGAACT 834
 DB 2862 CTGCGGCGAGGCGCTATGTAAGTGTGTTCCCTTCTGCGCACTGAGCGCGCGAGAACT 2921
 QY 835 ATCAGTAGACAGCTGCGCTTCCATGAAACGAAAAATTAATCATGTTTCTTAA 891
 DB 2922 ATCAGTAGACAGCTGCGCTTCCATGAAACGAAAAATTAATCATGTTTCTTAA 2978
 RESULT 5
 AB075680
 ID AB075680 standard; DNA; 55050 BP.
 AC AB075680;
 XX 11-NOV-2002 (first entry)
 DT 11-NOV-2002 (first entry)
 XX Human SEBK1 consensus genomic DNA.
 DE Human; SEBK1; chromosome 6p21; inflammatory disease; antiinflammatory;
 KW antiporiatic; gene therapy; gene; ds.
 XX Homo sapiens.
 OS
 XX MO200264831-A2.
 PN 22-AUG-2002.
 PD 13-FEB-2002; 2002WO-GB000653.
 XX 13-FEB-2001; 2001GB-00003514.
 PR 13-FEB-2001; 2001GB-00003514.
 XX (OXAG-) OXAGEN LTD.
 PA Lench NJ, Allen MJ, Nicholls RK,
 PI WPI; 2002-667013/71.
 DR
 XX
 PT Polymorphisms in the SEBK1 gene and polynucleotides encoding the SEBK1
 PT gene, for treating, diagnosing or determining susceptibility to SEBK1
 PT mediated disease, e.g. inflammatory disease such as psoriasis.
 XX
 PS Claim 4; Fig 2; 69pp; English.
 CC The present invention describes a polynucleotide (I) comprising: (a) a
 CC nucleic acid sequence (II) encoding the SEBK1 gene; (b) a nucleic acid
 CC sequence (III) encoding a fragment of the SEBK1 gene; or (c) a nucleic
 CC acid sequence (IV) that hybridises under stringent conditions to the
 CC polynucleotide of (II) or (III). (I) has antiinflammatory and
 CC antiporiatic activities and can be used in gene therapy. The alleles of
 CC one or more polymorphisms in the SEBK1 gene can be used for the
 CC manufacture of a medicament for the diagnosis and treatment of SEBK1
 CC mediated disease. SEBK1 protein fragments are useful in diagnostic,
 CC prognostic or therapeutic methods, or as research tools in drug
 CC screening. Human SEBK1 is located to chromosome 6p21. The present
 CC sequence represents a human SEBK1 nucleotide sequence
 XX
 SQ Sequence 55050 BP; 13076 A; 14198 C; 14560 G; 13197 T; 0 U; 19 Other;
 Query Match 87.0%; Score 775; DB 6; Length 55050;
 Best Local Similarity 99.7%; Pred. No. 7e-194;
 Matches 775; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 115 AGAGGATCTCCAGGCGAGGCGCACCTCTTCCACCCGAGAGAGAGAGAG 174
 DB 27096 ACAGGATCTCCAGGCGAGGCGCACCTCTTCCACCCGAGAGAGAGAGAG 27155
 QY 175 GCAGGCTCCCAACATTTGCTCAAGGCGCGCCCAAGTCCCGGTACCTTGGCCAGGAGCA 234

DB 27156 GCAGGCTCCCAACATTTGCTCAAGGCGCGCCCAAGTCCCGGTACCTTGGCCAGGAGCA 27215
 QY 235 CCCCTCTCTTTTAAAGATCTCCGCTTACCGGCCCAAGTCTCTGAGAGAGACTGCTT 294
 DB 27216 CCCCTCTCTTTTAAAGATCTCCGCTTACCGGCCCAAGTCTCTGAGAGAGACTGCTT 27275
 QY 295 GAAAGTGAAGTCTGAGCGCCCTGAAACCGCCCTGAAACGGAATCTCTTCAACTCCCGGCGCT 354
 DB 27276 GAAAGTGAAGTCTGAGCGCCCTGAAACCGCCCTGAAACGGAATCTCTTCAACTCCCGGCGCT 27335
 QY 355 GAGACCTTTGCGCGGAGAGACCCAGCCGCCAGAAAACCTTGAGCTCTGCGCTGAG 414
 DB 27336 GAGACCTTTGCGCGGAGAGACCCAGCCGCCAGAAAACCTTGAGCTCTGCGCTGAG 27395
 QY 415 GTGAGAACCGGACCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 474
 DB 27396 GTGAGAACCGGACCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 27455
 QY 475 TGGAGTCCCTGAGCGGTTCTGTTCCAGGAGATCTCCAGGAGACCCAGCGGCTCTGAGCC 534
 DB 27456 TGGAGTCCCTGAGCGGTTCTGTTCCAGGAGATCTCCAGGAGACCCAGCGGCTCTGAGCC 27515
 QY 535 TGTGATTTCCCGTGAATTTCTTCCCAATTAAGCTATCTCTTAAACCTTCTCTCATTC 594
 DB 27516 TGTGATTTCCCGTGAATTTCTTCCCAATTAAGCTATCTCTTAAACCTTCTCTCATTC 27575
 QY 595 CTGCGTTTATTTGAAACCCGTAAGTGTGTTCTCAATTTCTTCTGCTCCCTCTGAGA 654
 DB 27576 CTGCGTTTATTTGAAACCCGTAAGTGTGTTCTCAATTTCTTCTGCTCCCTCTGAGA 27635
 QY 655 TCCATCTTAGTCTCAGATCCGCGCTTTTCTCTGACAGGCTAAGCTACTCTCTA 714
 DB 27636 TCCATCTTAGTCTCAGATCCGCGCTTTTCTCTGACAGGCTAAGCTACTCTCTA 27695
 QY 715 CCTGCGCTCCAGGCGCTGCGCCCACTACCTCCAGCCGCTTCTGCGCGCGGATCG 774
 DB 27696 CCTGCGCTCCAGGCGCTGCGCCCACTACCTCCAGCCGCTTCTGCGCGCGGATCG 27755
 QY 775 CTGCGGCGAGGCGCTATGTAAGTGTGTTCCCTTCCGACACTGAGCGCGCGAGAACT 834
 DB 27756 CTGCGGCGAGGCGCTATGTAAGTGTGTTCCCTTCCGACACTGAGCGCGCGAGAACT 27815
 QY 835 ATCAGTAGACAGCTGCTGCTTCCATGAAACGAAAAATTAATCATGTTTCTTAA 891
 DB 27816 ATCAGTAGACAGCTGCTGCTTCCATGAAACGAAAAATTAATCATGTTTCTTAA 27872
 RESULT 6
 AAH45310
 ID AAH45310 standard; DNA; 25235 BP.
 XX
 AC AAH45310;
 XX
 DT 01-OCT-2001 (first entry)
 XX
 DE Human SEBK1 DNA.
 XX
 KW Human; MHC S; major histocompatibility complex S; vulgar psoriasis;
 KW diagnosis; primer; SEBK1; HCR; a-helix coiled-coil rod homologue;
 KW polymorphism; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT exon 1..420
 FT /*tag= a
 FT intron 421..1281
 FT /*tag= b
 FT exon 1282..1405
 FT /*tag= c
 FT intron 1406..1601
 FT /*tag= d

```

FT exon 1602..1702
FT /*tag= e
FT intron 1703..2351
FT /*tag= f
FT exon 2352..2364
FT /*tag= g
FT intron 2365..6286
FT /*tag= h
FT exon 6287..6509
FT /*tag= i
FT intron 6510..10416
FT /*tag= j
FT exon 10417..10493
FT /*tag= k
FT intron 10494..14243
FT /*tag= l
FT exon 14244..14407
FT /*tag= m
FT intron 14408..14243
FT /*tag= n
FT exon 25190..25235
FT /*tag= o

XX WO200142458-A1.
XX 14-JUN-2001.
XX 06-DEC-2000; 2000WO-JP008624.
XX 06-DEC-1999; 99JP-00346867.
XX (INOKO/) INOKO H.
XX Inoko H, Tamiya G;
XX WPI; 2001-381680/40.
XX
XX New primer DNA, useful for detecting vulgar psoriasis.
XX Claim 1; Page 46-62; 106pp; Japanese.
XX
XX The invention relates to a method of diagnosing vulgar psoriasis using
XX primers based on the sequences of the human MHC S, SBEK1 and HCR genes.
XX By analysing the sequences of these genes in Japanese patients with
XX psoriasis and in normal subjects, it has been found that some of the
XX examined polymorphisms correlate significantly to the group of patients
XX with psoriasis. Vulgar psoriasis can therefore be diagnosed by analysing
XX these gene polymorphisms. The present sequence is the human SBEK1 gene
XX which was used to design primers for use in the invention
XX
XX Sequence 25235 BP; 5967 A; 6703 C; 6487 G; 6078 T; 0 U; 0 Other;
XX
XX Query Match 86.8%; Score 773.8; DB 4; Length 25235;
XX Best Local Similarity 99.7%; Pred. No. 1.1e-193;
XX Matches 775; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Db 1991 GAGACCCCTTGGCCGCGAGAGACCCCAAGCCCAAGAAAACCCCTGGCTCTGCCCCCTGAG 2050
Qy 415 GTGACAAACCGACCTCAGAGAGAGACCGACCTAGACCAACCCCGGGAAGAGTAGATTA 474
Db 2051 GTGACAAACCGACCTCAGAGAGAGACCGACCTAGACCAACCCCGGGAAGAGTAGATTA 2110
Qy 475 TGAGTCCCTCAGCCGTTCTGTTCCAGGATCTCCAGGACCCAGCCCTCCACCC 534
Db 2111 TGAGTCCCTCAGCCGTTCTGTTCCAGGATCTCCAGGACCCAGCCCTCTCCACCC 2170
Qy 535 TCTGATTCCTCGTGAATCTTCCCAATTAGCCATATCTCTTAAACCTTCTCATTC 594
Db 2171 TCTGATTCCTCGTGAATCTTCCCAATTAGCCATATCTCTTAAACCTTCTCATTC 2230
Qy 595 CTCGGTTTATTCGAAACCCGTAAGGTGTGTCTCAATATTTCTCTGCTCCCTGAGA 654
Db 2231 CTCGGTTTATTCGAAACCCGTAAGGTGTGTCTCAATATTTCTCTGCTCCCTGAGA 2290
Qy 655 TCCATCTTAGTCTCTCATCGCCGTTTCTCTGAGACGCTTAGCCCTACTCTGCTA 714
Db 2291 TCCATCTTAGTCTCTCATCGCCGTTTCTCTGAGACGCTTAGCCCTACTCTCTTA 2350
Qy 715 CCTGCTCCAGGCTCGGCCCACTACCTCCACCCGGTCTTCTGCGCGCGATCG 774
Db 2351 CCTGCTCCAGGCTCGGCCCACTACCTCCACCCGGTCTTCTGCGCGCGATCG 2410
Qy 775 CTGGGGCAGGCTTAGTGTACTGTGTTCCCTTCTGCACTGTGTGGCGGCGAGAACT 834
Db 2411 CTGGGGCAGGCTTAGTGTACTGTGTTCCCTTCTGCACTGTGTGGCGGCGAGAACT 2470
Qy 835 ATCAGTAGACAGCGCTTCCATGAAAGGAAAAATTAATCATGTTTCTTAA 891
Db 2471 ATCAGTAGACAGCGCTTCCATGAAAGGAAAAATTAATCATGTTTCTTAA 2527

RESULT 7
ACH72505
ID ACH72505 standard; DNA; 565 BP.
XX
XX ACH72505;
XX
XX 29-JUL-2004 (first entry)
XX
XX Human genome derived single exon probe #5700.
XX
XX Human; probe; ss; gene expression; single exon probe; microarray;
XX alternative splicing event; genomic alteration.
XX
XX Homo sapiens.
XX
XX US2003194704-A1.
XX
XX 16-OCT-2003.
XX
XX 03-APR-2002; 2002US-00029386.
XX
XX 03-APR-2002; 2002US-00029386.
XX
XX (PENN/) PENN S G.
XX (RANK/) RANK D R.
XX (HANZ/) HANZEL D K.
XX
XX Penn SG, Rank DR, Hanzel DK;
XX
XX WPI; 2004-119264/12.
XX
XX New human genome-derived single exon nucleic acid probes useful for human
XX gene expression analysis, for identifying or characterizing alternative
XX splicing events, for assessing genomic alterations or as tools for
XX surveying tissues.
XX
XX Claim 15; SEQ ID NO 5700; 80pp; English.

```


XX 20-JUL-2001; 2001WO-IB001903.
PF 28-JUL-2000; 2000US-0221607P.
XX 02-MAY-2001; 2001US-0287724P.
PR
XX (COMP-) COMPUGEN INC.
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
PI WPI; 2002-25383/30.
DR
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
XX Example 1; SEQ ID NO 5077; 47bp; English.
PS
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC) transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridizing selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcripts. The libraries may also be used as specialized mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
XX
SQ Sequence 60 BP; 11 A; 25 C; 5 G; 19 T; 0 U; 0 Other;
Query Match 6.7%; Score 60; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 522 GCCCTCTCCACCCCTGATTCGCCGTAATCTTCCCAATTGAGCTATCTCTTAACC 581
DB 1 GCCCTCTCCACCCCTGATTCGCCGTAATCTTCCCAATTGAGCTATCTCTTAACC 60
RESULT 11
AAZ17263
ID AAZ17263 standard; cDNA; 1337 BP.
XX
XX AAZ17263;
DT 12-OCT-1999 (first entry)
XX
XX Human gene expression product cDNA sequence SEQ ID NO:4735.
DE
XX
XX Human; gene; gene expression product; diagnosis; therapy; probe;
KW detection; mapping; tissue typing; profiling; forensic; cancer;
KW genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
XX
XX Homo sapiens.
OS
XX
XX MO9938972-A2.
PN
XX 05-AUG-1999.
PD

XX 28-JAN-1999; 99MO-US001619.
XX
XX 28-JAN-1999; 98US-0072910P.
PR 24-FEB-1998; 98US-0075954P.
PR 31-MAR-1998; 98US-0080114P.
PR 03-APR-1998; 98US-0080515P.
PR 03-APR-1998; 98US-0080666P.
PR 21-OCT-1998; 98US-0105234P.
PR 28-OCT-1998; 98US-0105877P.
XX
XX (CHIR) CHIRON CORP.
PA (HYSE-) HYSEO INC.
XX
XX Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
PI Lamson G, Drmanac R, Ckvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones WL, Steacie-Crain B;
XX
XX WPI; 1999-494092/41.
DR
XX
XX Novel human genes and their expression products which are differentially
PT expressed in different cell types.
PT
XX
XX Claim 1; Page 2250-2251; 2479pp; English.
PS
XX The present invention describes a library of human polynucleotides
CC comprising the sequences given in AAZ12532 to AAZ17779. Also described is
CC a method of detecting differentially expressed genes correlated with the
CC cancerous state of a mammalian cell, comprising detecting at least one
CC differentially expressed gene product in a test sample from a cell
CC suspected of being cancerous, where the gene product is encoded by one of
CC the 5248 polynucleotide sequences given in AAZ12532 to AAZ17779. The
CC polynucleotides can be used as a source of primers and probes, which can
CC be used for a variety of purpose, e.g. detection of expression levels,
CC mapping, tissue typing or profiling, forensics, genetic analysis and
CC detection of polymorphisms. Polypeptides encoded by the polynucleotides
CC can be used for raising antibodies for experimental, diagnostic and
CC therapeutic purposes. The polynucleotides may also be used to construct
CC arrays for diagnostics (which may be used to determine function of an
CC encoded protein); and to detect differences in expression levels between
CC two cells (e.g. to identify abnormal or diseased tissue in a human, to
CC identify a genetic predisposition or susceptibility to a disease such as
CC cancer). The polynucleotides of the invention are especially used in the
CC diagnosis, prognosis and management of colorectal cancer, breast cancer,
CC and lung cancer. The polynucleotides can also be used to screen for
CC peptide analogues and antagonists
XX
SQ Sequence 1337 BP; 42 A; 577 C; 27 G; 22 T; 0 U; 669 Other;
Query Match 6.2%; Score 55; DB 2; Length 1337;
Best Local Similarity 25.9%; Pred. No. 0.00032;
Matches 192; Conservative 0; Mismatches 549; Indels 1; Gaps 1;
QY 33 CCAACCCAGCTTTGGGGGCGAGTACATGATGCTCAACTGAGAGCTCTGAGGAT 92
DB 346 CANNCCCNCCNN 405
QY 93 CCGTGTCTTTTGGCTGCAACCAAGAGGATCTCAGGAGGAGGACCCCTTCAACC 152
DB 406 NNNCCCCCNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNNCCNN 465
QY 153 ACCCGCAGAGGACCGAGAGAGGAGGAGCTCCCAATTTGCTCAGAGGCCCCCAGTCC 212
DB 466 CCCCNN 525
QY 213 CGGTGACCTTTGGCCAGGAGGACCCCTCTCTTTGAAGATCTCGCGCTTACCGCCAG 272
DB 526 NCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 585
QY 273 TCGTCCCTTGAGAGAGCTGCTGAATCTGAGATCTGAGCCCTTGAACCGCTTGAAGAGGA 332
DB 586 CCGNNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCN 645

Qy 333 TCCTCTCAACCTCCCGGCTGACGACCTTGGCGGAGAGCCCGAGAAA 392
 Db 646 NCCCCCCCCCCCCCCCCCCCCNNCNCNCCCCCCCCNNCNCNCCCCCCCCNNC 705
 Qy 393 CCCCT-GAGCTCTGCTGAGGTGAGCAACGAGCTCAGAGAGAGAGCTAGACC 451
 Db 706 CCCCCNNCNCNCCCCCCCCNNCNCNCCCCCCCCNNCNCNCCCCCCCCNNCNCN 765
 Qy 452 CACCCCGGAGAGTACAGATATGAGAGTCCCTCAGCCGTTCTGTTCCAGGATCTCC 511
 Db 766 NNCNCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 825
 Qy 512 AGGACCCAGCGCTCTGCAACCTCTGATTCGCCGTGAATCTTCCCAATTAGCCTATC 571
 Db 826 CANNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 885
 Qy 572 TCCTTAACCTCTTCTCATTTCCCTGAGTTTATTTGAAACCGTAAGGTGTTCTCA 631
 Db 886 NNCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 945
 Qy 632 ATATTCTCTGCTCCCTCTGAGATCATCTTACTCTCAGATGCGCGTTTCTCTCT 691
 Db 946 NCCNNNNNNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 1005
 Qy 692 GACAGCCTAAGCTACTCTCTCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 751
 Db 1006 NCCNNNNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 1065
 Qy 752 CGGCTCTCTGCGCGCGGATC 773
 Db 1066 CCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 1087

RESULT 12
 AAA02488/c
 ID AAA02488 standard; cDNA; 1218 BP.

XX AAA02488;

XX 19-MAY-2000 (first entry)

DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2479.

XX Human; colon cancer; tumour; diagnosis; gene expression product; probe;
 KW detection; cancerous state; metastasis; identification; breast cancer;
 KW oestrogen receptor-positive breast cancer; therapy;
 KW oestrogen receptor-negative breast cancer; lung cancer; ss.

XX Homo sapiens.

OS Homo sapiens.

PN W09958675-A2.

PD 18-NOV-1999.

PF 13-MAY-1999; 99WO-US010602.

PR 14-MAY-1998; 98US-0085426P.

PR 15-MAY-1998; 98US-0085537P.

PR 21-OCT-1998; 98US-0105234P.

PR 27-OCT-1998; 98US-0105877P.

PI (CHIR) CHIRON CORP.
 PI (HYSR-) HYSR INC.

PI Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
 PI Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
 PI Lamson G, Dzmanac R, Crtvenjakov R, Dickson M, Dzmanac S, Labat I;
 PI Lezhkowitz D, Kita D, Garcia V, Jones LM, Staehle-Crain B;
 DR WPI; 2000-126369/11.

PT Polynucleotide library used to determine cancerous states of mammalian
 PT cells.
 XX Claim 1; Page 995-996; 1097pp; English.

XX AAA00010 to AAA02716 represent polynucleotides isolated from cDNA
 CC libraries constructed from human colon cancer cell lines. The present
 CC invention also describes a method of detecting differentially expressed
 CC genes correlated with a cancerous state of a mammalian cell, comprising
 CC detecting at least one differentially expressed gene product in a test
 CC sample derived from a cell suspected of being cancerous, where detection
 CC of the differentially expressed gene product is correlated with a
 CC cancerous state of the cell from which the test sample was derived. The
 CC polynucleotide sequences can be used in a method for detecting
 CC differentially expressed genes correlated with a cancerous state of a
 CC mammalian cell. The polynucleotides can also be used as probes for
 CC detecting and mapping related genes. They can be used in diagnosis and
 CC prognosis of diseases and disorders (e.g. identification of pre-
 CC metastatic or metastatic cancerous states, stages of cancer, or
 CC responsiveness of cancer to therapy). This is particularly for breast
 CC cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
 CC negative breast cancer, lung cancer, and colon cancer.

XX Sequence 1218 BP; 9 A; 31 C; 494 G; 37 T; 0 U; 647 Other;

Query Match 5.9%; Score 53; DB 3; Length 1218;
 Best Local Similarity 24.0%; Pred. No. 0.0011;
 Matches 155; Conservative 0; Mismatches 492; Indels 0; Gaps 0;

Qy 106 CTGACACAGAGGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 165
 Db 1070 CANNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 1011
 Qy 166 CGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 225
 Db 1010 NNNNNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 951
 Qy 226 CCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 285
 Db 950 CCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 891
 Qy 286 GACCTGCTGAACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 345
 Db 890 NNNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 831
 Qy 346 CCCCCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 405
 Db 830 CCCCCCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 771
 Qy 406 GCCCTGAGGTGAGCAACGAGCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 465
 Db 770 NNNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 711
 Qy 466 TACAGATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 525
 Db 710 NCCNNNNNNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 651
 Qy 526 TCTCAGCTCTGATTTCCCGTGAATTTCTTCCCAATTAGCTATCTCTTAACTCTT 585
 Db 650 NNNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 591
 Qy 586 CTCTATTCCTGCTGTTTATTTGAAACCGTGAAGGTGTTTCTGCAATATTTCTGTC 645
 Db 590 NNNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 531
 Qy 646 CTCTGAGATCATCTTACTGCTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 705
 Db 530 CCCCCNNNNNNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 471
 Qy 706 ACTCTCTACTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 752
 Db 470 CCCCCCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 424

CC host cells comprising the fusion promoters, a method of identifying genes
 CC involved in cellular proliferation or required for proliferation of a
 CC prokaryotic cell using the vector, a method of identifying compounds that
 CC inhibit the proliferation of a prokaryotic cell using the vector, a
 CC method of identifying a compound that reduces the activity or level of a
 CC gene product required for proliferation of a cell using the vector, a
 CC compound identified by the methods, a method of inhibiting the activity
 CC or expression of a gene in an operon required for proliferation using the
 CC vector, manufacturing an antibiotic comprising using the vector or cell
 CC and identifying a nucleic acid with promoter activity in *Enterococcus*
 CC faecalis. The fusion promoters are useful for regulating nucleic acid or
 CC polypeptide expression, particularly for regulating gene expression in
 CC bacteria and for identifying proliferation-regulated genes or molecules
 CC with potential antibiotic activity. The modified promoters are also
 CC useful for replacing endogenous promoters to create cells with specific
 CC regulatable genes. The present sequence is vector (or fragment)
 CC incorporating a fusion promoter sequence of the invention
 CC
 SQ Sequence 12733 BP; 3549 A; 2567 C; 3207 G; 3409 T; 0 U; 1 Other;

Query Match 5.8%; Score 51.8; DB 6; Length 12733;
 Best Local Similarity 42.2%; Pred. No. 0.0048;

Matches 293; Conservative 0; Mismatches 402; Indels 0; Gaps 0;

QY 75 CTGGAGCTCTCGGGAGTCTGTCCTTGGCTGCACACGAGCATCTCAGGACGGA 134
 DB 5473 CTGCGGACACTGTCTTCAAGATTGATGAAGAGACGTATAGTGGCGACGA 5414
 QY 135 GGGGCACTCTTCACCCGACCGGAGAGACGAGAGGAGGAGGCTCCCAATTGCC 194
 DB 5413 TAGTCATGCCCCGCGCCACCGAAGAGCTGACTGGGTTGAAGGCTCTCAAGGCGATCG 5354
 QY 195 TCAAGGCCCCCGGAGTCTCCGCGTACCTTGGCCAGGGGCACTCTCTTTGAAGATCC 254
 DB 5353 GTGACCC 5294
 QY 255 TCCGCTACCCGCGCCGATGTCCTGTGAGAGACCTGCTTAAGTGGAGTGGCCCC 314
 DB 5293 CCC 524
 QY 315 TGAACGCGCTAGAAAGGATCTCTCAACCTCCCGGCTGAGCAGCTTGGCGGAGG 374
 DB 5233 CCC 5174
 QY 375 ACCCGACCCCGGAGAAAACCTTGGCTCTGCTGAGTGAAGCAACGACCTCAGGA 434
 DB 5173 CCC 5114
 QY 435 GGAGCGAGCACTAGACCAACCGGGAAGATGATGAGTGGCTCAGCGTTC 494
 DB 5113 CCC 5054
 QY 495 TGTTCGAGGATCTCAGGACCAAGCCCTCTCAACCTTGAATTCGCCGTAATTC 554
 DB 5053 CCC 4994
 QY 555 TCCCAATTAGCTATCTCTTAACCTTTCGATTCCTGGGTTTATTTGAACCC 614
 DB 4993 CCC 4934
 QY 615 GTAAGTGTGTCTCAATATTTCTGATCCCTCTGAGATGATGATGATCTCAAT 674
 DB 4933 CCC 4874
 QY 675 CGCCCGTTTTTCTCTGACAGCTTAAGCTACTCTCTAAGCTCAGGCTCGGC 734
 DB 4873 CCC 4814
 QY 735 CCGACCTACTCTCAACCGGATCTTCTGCGCGGC 769
 DB 4813 CCC 4779

RESULT 15

ACD13882/c
 ID ACD13882 standard; DNA; 12733 BP.

XX ACD13882;

XX 15-AUG-2003 (first entry)

XX L. lactis promoter containing plasmid pBPER14.

XX Promoter; ds; gram positive bacteria; *Staphylococcus aureus*; plasmid;
 XX *Enterococcus faecalis*; operator; xyfO; tetO; trpO; malO; lambda-clO;
 XX cellular proliferation.

XX *Lactococcus lactis*.

OS Synthetic.

XX US2003027286-A1.

XX 06-FEB-2003.

XX 21-DEC-2001; 2001US-00032393.

XX 06-SEP-2000; 2000US-0230335P.

XX 27-DEC-2000; 2000US-0259434P.

XX (HASELBECK R.

XX (WALL D.

XX (GROSS M.

XX Haseelbeck R, Wall D, Gross M;

XX WPI: 2003-479541/45.

XX New isolated nucleic acid comprising a fusion promoter having at least
 XX one promoter that is modified to have altered activity in at least one
 XX gram-positive organism, useful for regulating gene expression in
 XX bacteria.

XX Example 3; Page 86-92; 142pp; English.

XX The invention relates to an isolated nucleic acid comprising a fusion
 XX promoter having at least one promoter that is modified to have altered
 XX activity in at least one gram-positive organism (e.g. *Staphylococcus*
 XX *aureus* or *Enterococcus faecalis*). The promoter is linked to at least one
 XX operator selected from xyfO, tetO, trpO, malO and lambda-clO, which are
 XX positioned such that the binding of at least one repressor to the
 XX operator represses transcription from the fusion promoter. Also included
 XX are a vector comprising the isolated nucleic acid, a host cell comprising
 XX the nucleic acid. The fusion promoter is useful for identifying genes
 XX involved in cellular proliferation, identifying a compound that reduces
 XX the activity or level of a gene product required for proliferation of a
 XX cell, inhibiting the activity or expression of a gene in an operon
 XX required for proliferation, manufacturing an antibiotic, identifying a
 XX gene that is required for proliferation of a prokaryotic cell,
 XX identifying a compound that inhibits the proliferation of a prokaryotic
 XX cell and regulating gene expression in bacteria. The present sequence is
 XX a plasmid containing a fusion promoter of the invention
 XX

SQ Sequence 12733 BP; 3549 A; 2567 C; 3207 G; 3409 T; 0 U; 1 Other;

Query Match 5.8%; Score 51.8; DB 9; Length 12733;
 Best Local Similarity 42.2%; Pred. No. 0.0048;

Matches 293; Conservative 0; Mismatches 402; Indels 0; Gaps 0;

QY 75 CTGGAGCTCTCGGGAGTCTGTCCTTGGCTGCACACGAGCATCTCAGGACGGA 134
 DB 5473 CTGCGGACACTGTCTTCAAGATTGATGAAGAGACGTATAGTGGCGACGA 5414
 QY 135 GGGGCACTCTTCACCCGACCGGAGAGACGAGAGGAGGAGGCTCCCAATTGCC 194
 DB 5413 TAGTCATGCCCCGCGCCACCGAAGAGCTGACTGGGTTGAAGGCTCTCAAGGCGATCG 5354

QY 195 TCAGGGCCCCCAGTCCCGGAGACCTTGGCAGGGGCACCCCCTCTTTGAAGATCC 254
 Db 5353 GTGACCC 5294
 QY 255 TCCGCGCTAACCGCCCGCACTGCTCTGAGAGACCTGCTGAACCTGAGCTTGCCCCC 314
 Db 5293 CC 5234
 QY 315 TGAACCGCTGAAAGGATCCTCTCAACCTCCCGGCTGAGACCTTGGCCGAGG 374
 Db 5233 CC 5174
 QY 375 ACCCGAGCCCCCAGAAAAACCTGCGCTCTGCTGAGGTGAGCAACGACCTCAGGA 434
 Db 5173 CC 5114
 QY 435 GGAAGCAGACCTTAACCCCGGAGAGATACAGATATGAGTCCCTCAGCCGTTG 494
 Db 5113 CC 5054
 QY 495 TGTCCAGGATCTCCAGGACCCAGCCCTCTCAACCTTGATTCGCCGATTTCT 554
 Db 5053 CC 4994
 QY 555 TCCCAATTAGCTATCTCTTAACCTCTCTCATTCCTGAGTTTAATCTGAACC 614
 Db 4993 CC 4934
 QY 615 GTAAGTGTGTCTCAATATTCTGTCCCTCTGAGATCCATTAAGTCTCAT 674
 Db 4933 CC 4874
 QY 675 CGCCGTTTTTCTCTGACAGCCTTAAGCTACTCTCTAAGCTTCCAGGCTGAGC 734
 Db 4873 CC 4814
 QY 735 CCAAGCTACTCCAGCCCGGCTTCTGCGCGGC 769
 Db 4813 CC 4779

Search completed: January 11, 2005, 07:08:39
 Job time : 545 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 11, 2005, 06:08:48 ; Search time 4034 Seconds
(without alignments)
10444.998 Million cell updates/sec

Title: US-09-994-365-1
Perfect score: 891
Sequence: 1 ccccttgggggtccacagca.....taaaatcatgtcttcttaa 891

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb ba: *
2: gb htg: *
3: gb_in: *
4: gb_cm: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_dr: *
10: gb_ro: *
11: gb_sta: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	891	100.0	891	6	AX477387 Sequence
2	889.4	99.8	1143	6	CO722444 Sequence
3	889.4	99.8	1185	9	AF484420 Sequence
4	886.2	99.5	1473	6	AX406002 Sequence
5	883	99.1	1143	9	AB031480 Sequence
6	775.4	87.0	2997	6	AX477396 Sequence
7	775.4	87.0	3001	6	AX477390 Sequence
8	775.4	87.0	40878	6	AC004195 Homo sapi
9	775	87.0	55050	6	AX522117 Sequence
10	773.8	86.8	25235	6	BD095297 The metho
11	773.8	86.8	30911	9	AB088114 Homo sapi
12	773.8	86.8	39196	9	AB023060 Homo sapi
13	773.8	86.8	70288	9	AL662867 Human DNA
14	773.8	86.8	99999	9	AP000510 Human sapi
15	773.8	86.8	135396	9	BX927139 Human sapi
16	770.6	86.5	204298	9	AL662844 Human DNA
17	763.4	85.7	113388	9	AL773544 Human DNA
18	757.8	85.1	300050	9	AB100083 Pan trogl
19	708.6	79.5	200068	9	AC148691 Macaca mu

C	20	700.8	78.7	175689	9	AC148703	AC148703 Macaca mu
C	21	557.8	62.6	349980	6	AX344554	AX344554 Sequence
C	22	370.4	41.6	154749	4	AB113354	AB113354 Sus scrof
C	23	348.2	39.1	349980	6	AX344570	AX344570 Sequence
C	24	303.6	34.1	383	4	AF484422	AF484422 Sus scrof
C	25	288.6	32.4	388	9	HS114A35	HS114A35 Human HLA C
C	26	262.6	29.5	809	10	AF484421	AF484421 Mus muscu
C	27	245.8	27.6	773	10	AF159091	AF159091 Mus muscu
C	28	234.4	26.3	1377	10	AF159090	AF159090 Mus muscu
C	29	234.4	26.3	159179	10	MMHC322F16	AF111103 Mouse maj
C	30	234.4	26.3	226594	10	AC087216	AC087216 Mus muscu
C	31	231.6	26.0	349571	1	BM883047	BM883047 Rattus no
C	32	160	18.0	248	6	AR418279	AR418279 Sequence
C	33	160	18.0	248	6	AX978973	AX978973 Sequence
C	34	160	18.0	248	6	BD113832	BD113832 EST and e
C	35	120	13.5	16887	9	AL662833	AL662833 Human DNA
C	36	80.8	9.1	7218	6	166494	166494 Sequence 14
C	37	65.8	7.4	250	9	HS114A26	HS114A26 Human HLA C
C	38	65.2	7.3	202083	2	AC023833	AC023833 Mus muscu
C	39	62.8	7.0	56970	2	AC138096	AC138096 Homo sapi
C	40	62.6	7.0	302176	2	AC096479	AC096479 Rattus no
C	41	62.6	7.0	303091	2	AC084799	AC084799 Mus muscu
C	42	61.8	6.9	3133	6	AX646999	AX646999 Sequence
C	43	61.8	6.9	298166	2	AC087563	AC087563 Homo sapi
C	44	61.4	6.9	75863	2	AC016059	AC016059 Homo sapi
C	45	61.4	6.9	205691	2	AC087227	AC087227 Mus muscu

ALIGNMENTS

RESULT 1	AX477387	891 bp	DNA	linear	PAT 12-AUG-2002
LOCUS	AX477387	Sequence 1 from Patent WO024375.			
DEFINITION	AX477387				
ACCESSION	AX477387.1	GI:22216617			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM		Homo sapiens (human)			
REFERENCE					
AUTHORS		Charley, P., Moss, P. and Mceuen, M.			
TITLE		Compositions and methods for diagnosing or treating psoriasis			
JOURNAL		Patent: WO 024375-A 1 06-JUN-2002;			
FEATURES		Celltech R & D, Inc. (US)			
source		Location/Qualifiers			
		1..891			
		/organism="Homo sapiens"			
		/mol_type="unassigned DNA"			
		/db_xref="taxon:9606"			
		64..474			
		/note="unnamed protein product"			
		/codon_start=1			
		/protein_id="CAD43680.1"			
		/db_xref="GI:22216618"			
		/translation="MILNKLGLIVLCLHTRGISGSEGRPSHPADREASPTLP			
		QGPVGVDPWPAPLFEDEPTPRSPRPMWDLPELGVWPEPRTPDPPRDEPWP			
		AGQPENPWPAPVEVDNRPQERPDIDPREEYR"			
ORIGIN					
Query Match		100.0%; Score 891; DB 6; Length 891;			
Best Local Similarity		100.0%; Pred. No. 2.6e-192; Index 0; Gaps 0;			
Matches		891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	CCCTTTGGGGTCCAGCAGCCAGCTCAGCCACCCAGCTTTGGGGCCAGTACATA	60		
Db	1	CCCTTTGGGGTCCAGCAGCCAGCTCAGCCACCCAGCTTTGGGGCCAGTACATA	60		
Qy	61	GCGATGATCTCTCACTGAGAGCTCTGGGGATCTCTTGGCTGTGCACACAGAGGC	120		
Db	61	GCGATGATCTCTCACTGAGAGCTCTGGGGATCTCTTGGCTGTGCACACAGAGGC	120		

QY 121 ATCTCAGGACGAGGAGGACCCCTCTCACCACCCGAGAGACCGAGAGAGGAGGAC 180
 DB 121 ATCTCAGGACGAGGAGGACCCCTCTCACCACCCGAGAGACCGAGAGAGGAGGAC 180
 QY 181 TCCCAACATTGCTCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
 DB 181 TCCCAACATTGCTCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
 QY 241 CTCTTTGAAGATCTCTCCGCTTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
 DB 241 CTCTTTGAAGATCTCTCCGCTTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
 QY 301 GAGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
 DB 301 GAGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
 QY 361 CTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
 DB 361 CTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
 QY 421 AACGAGCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
 DB 421 AACGAGCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
 QY 481 CCGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
 DB 481 CCGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
 QY 541 TCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
 DB 541 TCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
 QY 601 TTTATTTGAAACCGGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
 DB 601 TTTATTTGAAACCGGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
 QY 661 CTTAAGTCTCAATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
 DB 661 CTTAAGTCTCAATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
 QY 721 CTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
 DB 721 CTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
 QY 781 CAGGAGCTATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 840
 DB 781 CAGGAGCTATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 840
 QY 841 AGACAGCTGCTGCTTCCATGAAACGAAATTAATCAATGTTTCTTAA 891
 DB 841 AGACAGCTGCTGCTTCCATGAAACGAAATTAATCAATGTTTCTTAA 891

RESULT 2
 LOCUS C0722444 1143 bp DNA linear PAT 03-FEB-2004
 DEFINITION Sequence 8378 from Patent WO20068579.
 ACCESSION C0722444
 VERSION C0722444.1 GI:42283301
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Venter, C.J., Adams, M.C., Li, P.W., and Myers, E.W.
 Kites, such as nucleic acid arrays, comprising a majority of
 humamexons or transcripts, for detecting expression and other uses
 thereof
 Patent: WO 02068579-A 8378 06-SEP-2002;
 PE Corporation (NY) (US)
 Location/Qualifiers

source 1..1143
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 99.9%; Score 889.4; DB 6; Length 1143;
 Best Local Similarity 99.9%; Pred. No. 5,9e-192;
 Matches 890; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ORIGIN
 1 CTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60
 253 CTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
 61 GCGATATCTCTCAATCTGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
 313 GCGATATCTCTCAATCTGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
 121 ATCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
 373 ATCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
 181 TCCCAACATTGCTCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
 433 TCCCAACATTGCTCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
 241 CTCTTTGAAGATCTCTCCGCTTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
 493 CTCTTTGAAGATCTCTCCGCTTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
 301 GAGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
 553 GAGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
 361 CTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
 613 CTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 421 AACGAGCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
 673 AACGAGCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
 481 CCGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
 733 CCGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
 541 TCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
 793 TCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
 601 TTTATTTGAAACCGGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
 853 TTTATTTGAAACCGGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
 661 CTTAAGTCTCAATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
 913 CTTAAGTCTCAATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
 721 CTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
 973 CTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
 781 CAGGAGCTATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1620
 1033 CAGGAGCTATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 1680
 841 AGACAGCTGCTGCTTCCATGAAACGAAATTAATCAATGTTTCTTAA 891
 1093 AGACAGCTGCTGCTTCCATGAAACGAAATTAATCAATGTTTCTTAA 1143

RESULT 3
 AF484420

LOCUS AF484420 1185 bp mRNA linear PRI 02-MAR-2003
DEFINITION Homo sapiens psoriasis susceptibility 1 candidate 2 (PSORS1C2)
ACCESSION AF484420
VERSION AF484420.1 GI:28628834
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1185)
AUTHORS Holm,S.J., O'Brien,K.P., Carlen,L. and Stahle-Backdahl,M.
TITLE The PSORS1C1 and PSORS1C2 genes in 6p21.3 associate strongly with
psoriasis in the Swedish population
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1185)
AUTHORS Holm,S.J., O'Brien,K.P., Carlen,L. and Stahle-Backdahl,M.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-2002) Dermatology, Karolinska Institute, L8:02
Karolinska Sjukhuset, Stockholm S-17176, Sweden
FEATURES
source location/Qualifiers
1..1185
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
/label_type="skin"
1..1185
/gene="PSORS1C2"
325..735
/gene="PSORS1C2"
/codon_start=1
/product="psoriasis susceptibility 1 candidate 2"
/protein_id="AA049377.1"
/db_xref="GI:28628835"
/translation="MILNWKILGILVCLHTRGISGSEGHSPHPADREAGSPPLP
QGPVPDPMWPGAPLPEDPPTPRSPRPMWDLPTGTWVPEPPTDPPQPRDDPMP
AGQPPENPMPAPPEVDNRPQEBPDLDPREBYR"
ORIGIN
Query Match 99.8%; Score 889.4; DB 9; Length 1185;
Best Local Similarity 99.9%; Pred. No. 5.9e-192;
Matches 890; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCTTTGGGGTTCCCAAGGACCACTCAAGCCCAACCCAGCTTTGGGGGCCAGTACATA 60
DB 262 CTTCTGGGGTTCCCAAGGACCACTCAAGCCCAACCCAGCTTTGGGGGCCAGTACATA 321
QY 61 GCCATGATCCCACTGGAAGCTCTGGGGAATCTGTGCTTTGCTGACACACAGAGGC 120
DB 322 GCCATGATCCCACTGGAAGCTCTGGGGAATCTGTGCTTTGCTGACACACAGAGGC 381
QY 121 ATCTCAGGACGAGGACCACTCTCAACCCAGGACGAGACGAGAGGAGGAGGC 180
DB 382 ATCTCAGGACGAGGACCACTCTCAACCCAGGACGAGACGAGAGGAGGAGGC 441
QY 181 TCCCAACATTGCTCTCAGAGGCCCTCCAGTCCCGGTGACCTTTGGCCAGGGGCAACCCCT 240
DB 442 TCCCAACATTGCTCTCAGAGGCCCTCCAGTCCCGGTGACCTTTGGCCAGGGGCAACCCCT 501
QY 241 CTTCTTAAAGATCTCTCCGCTCAACCCGCGGACGAGTGTCTCCGAGAGACCTGCCTGAAC 300
DB 502 CTTCTTAAAGATCTCTCCGCTCAACCCGCGGACGAGTGTCTCCGAGAGACCTGCCTGAAC 561
QY 301 GAGATCTGAGCCCTCTGAACCGCTAGAACGATCTCTCAACTCCCGGCTGAGAGAC 360
DB 562 GAGATCTGAGCCCTCTGAACCGCTAGAACGATCTCTCAACTCCCGGCTGAGAGAC 621
QY 361 CTTTGGCCGAGAGACCCCAAGAACCCCTGAGCTCTGCTGCTGAGGTGAGC 420
DB 622 CTTTGGCCGAGAGACCCCAAGAACCCCTGAGCTCTGCTGCTGAGGTGAGC 681

QY 421 AACGACCTCAGAGAGAGAGCCAGACTAGACCCACCCGGAGAGATACAGATATGAGT 480
DB 682 AACGACCTCAGAGAGAGAGCCAGACTAGACCCACCCGGAGAGATACAGATATGAGT 741
QY 481 CCCCTCAGCGGTTCTGTTCCCAAGGCATCTCAGGACCAACGCCCTCTCAACCTTGAT 540
DB 742 CCCCTCAGCGGTTCTGTTCCCAAGGCATCTCAGGACCAACGCCCTCTCAACCTTGAT 801
QY 541 TCCCGGTAATCTTCCCAATTTAGCTATCTCTTAAACCTTCTTCCATTCCTCGGT 600
DB 802 TCCCGGTAATCTTCCCAATTTAGCTATCTCTTAAACCTTCTTCCATTCCTCGGT 661
QY 601 TTTATTTGAACCCGTAGAGGTGATCTCAATATTTCTGTCGCCCTCTGAGATCCATA 660
DB 862 TTTATTTGAACCCGTAGAGGTGATCTCAATATTTCTGTCGCCCTCTGAGATCCATA 921
QY 661 CTTATGCTCAATCGCCGCTTTTCTCTGACAGCTTAAAGCTTACTCTCACTGCGC 720
DB 922 CTTATGCTCAATCGCCGCTTTTCTCTGACAGCTTAAAGCTTACTCTCACTGCGC 981
QY 721 CTCAGGCTCGGCGCCCACTACCTCCACCCGCTTCTGCGCGGCGATGCTGAGG 780
DB 982 CTCAGGCTCGGCGCCCACTACCTCCACCCGCTTCTGCGCGGCGATGCTGAGG 1041
QY 781 CAGGCTATGATGATCTGATCTCTTCTGACCACTGATGCGCGGCGAGAACTATCAGT 840
DB 1042 CAGGCTATGATGATCTGATCTCTTCTGACCACTGATGCGCGGCGAGAACTATCAGT 1101
QY 841 AGACAGCTGCTGCTTCATGAAACGAAATATATATATATATATATATATATATAT 891
DB 1102 AGACAGCTGCTGCTTCATGAAACGAAATATATATATATATATATATATATATAT 1152
RESULT 4
AX406002
LOCUS AX406002 1473 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 417 from Patent WO0222660.
ACCESSION AX406002
VERSION AX406002.1 GI:21439443
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Tang,Y.T., Liu,C., Zhou,P., Asundi,V., Zhang,J., Zhao,Q.A., Ren,F.,
Xue,A.J., Yang,Y., Wehrman,T. and Drmanac,R.T.
TITLE Novel nucleic acids and polypeptides
JOURNAL Patent: WO 0222660-A 417 21-MAR-2002;
HYSBO, INC. (US)
FEATURES
source location/Qualifiers
1..1473
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
636..1046
/note="unamed protein product"
/codon_start=1
/protein_id="CAD35109.1"
/db_xref="GI:21439444"
/translation="MILNWKILGILVCLHTRGISGSEGHSPHPADREAGSPPLP
QGPVPDPMWPGAPLPEDPPTPRSPRPMWDLPTGTWVPEPPTDPPQPRDDPMP
AGQPPENPMPAPPEVDNRPQEBPDLDPREBYR"
ORIGIN
Query Match 99.5%; Score 886.2; DB 6; Length 1473;
Best Local Similarity 99.7%; Pred. No. 3.1e-191;
Matches 888; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCTTTGGGGTTCCCAAGGACCACTCAAGCCCAACCCAGCTTTGGGGGCCAGTACATA 60
DB 573 CTTCTGGGGTTCCCAAGGACCACTCAAGCCCAACCCAGCTTTGGGGGCCAGTACATA 632

```

QY 61 GCCATGATCTCACTGGAAGCTCTGGGATCTGCTCTTGGCTGACACCAAGAGGC 120
DB 633 GCGATGATCTCACTGGAAGCTCTGGGATCTGCTCTTGGCTGACACCAAGAGGC 692
QY 121 ATCTCAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
DB 693 ATCTCAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 752
QY 181 TCCCAACATTTGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
DB 753 TCCCAACATTTGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 812
QY 241 CTCTTTGAAGATCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
DB 813 CTCTTTGAAGATCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 872
QY 301 GGAATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB 873 GGAATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 932
QY 361 CTTTGGCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
DB 933 CTTTGGCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 992
QY 421 AACGACCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
DB 993 AACGACCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1052
QY 481 CCCCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
DB 1053 CCCCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1112
QY 541 TCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
DB 1113 TCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1172
QY 601 TTTATTTGGAACCGGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
DB 1173 TTTATTTGGAACCGGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1232
QY 661 CTTAGCTCTCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
DB 1233 CTTAGCTCTCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1292
QY 721 CTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
DB 1293 CTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1352
QY 781 CAGGAGCTATGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
DB 1353 CAGGAGCTATGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1412
QY 841 AGACAGCTGCTGCTTCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 891
DB 1413 AGACAGCTGCTGCTTCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1463

```

RESULT 5

```

LOCUS AB031480 1143 bp mRNA linear PRI 08-DEC-1999
DEFINITION Homo sapiens SPRI mRNA, complete cds.
ACCESSION AB031480
VERSION AB031480.1 GI:5539433
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE 1. Oka, A., Tamiya, G., Tomizawa, M., Oka, M., Katsuyama, Y., Makino, S.,
AUTHORS Kawakubo, Y., Sugai, J., Ozawa, A., Ohkido, M., Kimura, M., Bahram, S.
and Inoko, H.

```

TITLE Association analysis using refined microsatellite markers localizes a susceptibility locus for psoriasis vulgaris within a 111 kb segment telomeric to the HLA-C gene

JOURNAL Hum. Mol. Genet. 8 (12), 2165-2170 (1999)

MEDLINE -20044706

PUBMED 10545595

REFERENCE 2 (bases 1 to 1143)

AUTHORS Tamiya, G., Tomizawa, M., Makino, S., Oka, A., Nakajima, K., Kimura, M. and Inoko, H.

TITLE Direct Submision

JOURNAL Submitted (25-AUG-1999) Akira Oka, Tokai University School of Medicine, Division of Molecular Life Science, Bohseidai, Isehara, Kanagawa 259-1193, Japan (E-mail: oka246@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121 (ex.2579), Fax:81-463-94-8884)

FEATURES

source

1..1143

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/chromosome="6"

/map="6p21.3"

/sex="male"

/cell_type="epidermal keratinocytes"

1..1143

/gene="SPR1"

/gene="SPR1"

316..726

/gene="SPR1"

/codon_start=1

/protein_id="BA08131.1"

/db_xref="GI:5539434"

/translation="MLNKLGLIVLCHTRGISSEHPSHPADREAGSPPLP

OGPPVGDWPGAPLPEFEDPPRPSRPMDPECTGVWPPPEPRDPPQPPRDPDWP

AGQPENPMPPAPPEVDNRPQEBPDPPREYR"

ORIGIN

Query Match 99.1%; Score 883; DB 9; Length 1143;

Best Local Similarity 99.4%; Pred. No. 1,7e-190;

Matches 886; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

QY 1 CCGTTGGGGTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
DB 253 CCGTTGGGGTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 312
QY 61 GCCATGATCTCACTGGAAGCTCTGGGATCTGCTCTTGGCTGACACCAAGAGGC 120
DB 313 GCCATGATCTCACTGGAAGCTCTGGGATCTGCTCTTGGCTGACACCAAGAGGC 372
QY 121 ATCTCAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
DB 373 ATCTCAGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 432
QY 181 TCCCAACATTTGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
DB 433 TCCCAACATTTGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 492
QY 241 CTCTTTGAAGATCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
DB 493 CTCTTTGAAGATCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 552
QY 301 GGAATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB 553 GGAATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 612
QY 361 CTTTGGCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
DB 613 CTTTGGCCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 672
QY 421 AACGACCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
DB 673 AACGACCTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 732
QY 481 CCCCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540

```

Db 733 CCCCTCAGCGTCTGTCTCCAGGCATCTCCAGGACCCAGCCCTCTCCACCTCTGAT 792
Qy 541 TCCCGTGAATTTCTCCCAATTTAGCCATCTCTTAACCTCTTCCATTTCCCTGGGT 600
Db 793 TCCCGTGAATTTCTCCCAATTTAGCCATCTCTTAACCTCTTCCATTTCCCTGGGT 852
Qy 601 TTATATCTGAACCCGTAAGGTGTGTCTCAATATTTCTGTCCCTCTGAGATTCATA 660
Db 853 TTATATCTGAACCCGTAAGGTGTGTCTCAATATTTCTGTCCCTCTGAGATTCATA 912
Qy 661 CTATAGTCTCAATCGCCCGCTTTTCTCTGACAGCTTAAGCTTCTTACTCTGC 720
Db 913 CTATAGTCTCAATCGCCCGCTTTTCTCTGACAGCTTAAGCTTCTTACTCTGC 972
Qy 721 CTCAGGCTCTGCGCCCACTCACTCCAGCCGCTTCTGCGCGGCGATTCGCTGGG 780
Db 973 CTCAGGCTCTGCGCCCACTCACTCCAGCCGCTTCTGCGCGGCGATTCGCTGGG 1032
Qy 781 CAGGCTATGCTGATGTCTTCTCTGCACTGTGTGCGCGGCGAGAACTATGAT 840
Db 1033 CAGGCTATGCTGATGTCTTCTCTGCACTGTGTGCGCGGCGAGAACTATGAT 1092
Qy 841 AGACAGCTGCTGCTTCCATGAAACGAAATAAATATCATGTTTCTTAA 891
Db 1093 AGACAGCTGCTGCTTCCATGAAACGAAATAAATATCATGTTTCTTAA 1143
RESULT 6
AX477396 2997 bp DNA linear PAT 12-AUG-2002
LOCUS Sequence 10 from Patent WO244375.
DEFINITION AX477396
ACCESSION AX477396.1 GI:22216625
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Charney, P., Moss, P. and Mceuen, M.
TITLE Compositions and methods for diagnosing or treating psoriasis
JOURNAL Patent: WO 0244375-A 10 06-JUN-2002;
Celltech R & D, Inc. (US)
FEATURES
source Location/Qualifiers
1..2997
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 87.0%; Score 775.4; DB 6; Length 2997;
Best Local Similarity 99.9%; Pred. No. 4.9e-166;
Matches 776; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 115 AGAGCATCTCAGGACGAGGAGGACCCCTCTACCCACCCGAGAGACCGAGAGAG 174
Db 2198 ACAGGATCTCAGGACGAGGAGGACCCCTCTACCCACCCGAGAGACCGAGAGAG 2257
Qy 175 GCAAGCTCTCCCAACATTTGCTCAGAGGCCCCCAGTCTCCGCTGACCTTGGCCAGAGGCA 234
Db 2258 GCAAGCTCTCCCAACATTTGCTCAGAGGCCCCCAGTCTCCGCTGACCTTGGCCAGAGGCA 2317
Qy 235 CCCCCTCTCTTTGAAGTCTCTGCGCTTACCGGCGGCTGCTCTTGGAGAGACTTGGCT 294
Db 2318 CCCCCTCTCTTTGAAGTCTCTGCGCTTACCGGCGGCTGCTCTTGGAGAGACTTGGCT 2377
Qy 295 GAAAGTGAAGTCTGCGGCGGCTGAGACCGGCTTGAAGAGTCTCTCAACCTCCGCGCT 354
Db 2378 GAAAGTGAAGTCTGCGGCGGCTTGAAGACCGGCTTGAAGAGTCTCTCAACCTCCGCGCT 2437
Qy 355 GAGACCTTTGGCGGAGAGACCCGAGACCCGAGAGAAACCTTGGCTCTGCTGCTGAG 414
Db 2438 GAGACCTTTGGCGGAGAGACCCGAGACCCGAGAGAAACCTTGGCTCTGCTGCTGAG 2497

Qy 415 GTGACAAACGACCTCAGAGAGACGACCTAGACCCACCCGGAAGATACAGATA 474
Db 2498 GTGACAAACGACCTCAGAGAGACGACCTAGACCCACCCGGAAGATACAGATA 2557
Qy 475 TGAAGTCCCTCAGCGCTGTCTTCCAGGACATCTCCAGGACCCAGCCCTCTCAACC 534
Db 2558 TGAAGTCCCTCAGCGCTGTCTTCCAGGACATCTCCAGGACCCAGCCCTCTCAACC 2617
Qy 535 TCTGATTCCTGGAATTTCTCCCAATTTAGCTTATCTCTTAAACCTTCTTCAATTC 594
Db 2618 TCTGATTCCTGGAATTTCTCCCAATTTAGCTTATCTCTTAAACCTTCTTCAATTC 2677
Qy 595 CTGGTTTATTTGAACCCGTAAGGTGTGTCTCAATATTTCTGCTTCCCTCTGAGA 654
Db 2678 CTGGTTTATTTGAACCCGTAAGGTGTGTCTCAATATTTCTTCTTCCCTCTGAGA 2737
Qy 655 TCATATCTAGTCTCAATCGCCGCTTTTCTCTGACAGCTTAAGCTTACTCTCTA 714
Db 2738 TCATATCTAGTCTCAATCGCCGCTTTTCTCTGACAGCTTAAGCTTACTCTCTA 2797
Qy 715 CTTGCTCCAGGCTCTGCGCCCACTTCTCCGACCCGCTTCTGCGCGGCGATTCG 774
Db 2798 CTTGCTCCAGGCTCTGCGCCCACTTCTCCGACCCGCTTCTGCGCGGCGATTCG 2857
Qy 775 CTGGGAGGAGGCTATGCTGATGTCTTCTTCTGCACTGTGTGCGCGGCGGAGACT 834
Db 2858 CTGGGAGGAGGCTATGCTGATGTCTTCTTCTGCACTGTGTGCGCGGCGGAGACT 2917
Qy 835 ATCAGTAGACGCTGCTTCCATGAAACGAAATAAATATCATGTTTCTTAA 891
Db 2918 ATCAGTAGACGCTGCTTCCATGAAACGAAATAAATATCATGTTTCTTAA 2974
RESULT 7
AX477390 3001 bp DNA linear PAT 12-AUG-2002
LOCUS Sequence 4 from Patent WO244375.
DEFINITION AX477390
ACCESSION AX477390.1 GI:22216619
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Charney, P., Moss, P. and Mceuen, M.
TITLE Compositions and methods for diagnosing or treating psoriasis
JOURNAL Patent: WO 0244375-A 4 06-JUN-2002;
Celltech R & D, Inc. (US)
FEATURES
source Location/Qualifiers
1..3001
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 87.0%; Score 775.4; DB 6; Length 3001;
Best Local Similarity 99.9%; Pred. No. 4.9e-166;
Matches 776; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 115 AGAGCATCTCAGGACGAGGAGGACCCCTCTACCCACCCGAGAGACCGAGAGAG 174
Db 2202 ACAGGATCTCAGGACGAGGAGGACCCCTCTACCCACCCGAGAGACCGAGAGAG 2261
Qy 175 GCAAGCTCTCCCAACATTTGCTCAGAGGCCCCCAGTCTCCGCTGACCTTGGCCAGAGGCA 234
Db 2262 GCAAGCTCTCCCAACATTTGCTCAGAGGCCCCCAGTCTCCGCTGACCTTGGCCAGAGGCA 2321
Qy 235 CCCCCTCTCTTTGAAGTCTCTGCGCTTACCGGCGGCTGCTCTTGGAGAGACTTGGCT 294
Db 2322 CCCCCTCTCTTTGAAGTCTCTGCGCTTACCGGCGGCTGCTCTTGGAGAGACTTGGCT 2381

QY 295 GAAATGAGTGTGGCCCCCTGAAACCGCTAGAAAGGATCTCTCAACTCCCGGCT 354
 Db 2382 GAAATCTGAGTGTGGCCCCCTGAAACCGCTAGAAAGGATCTCTCAACTCCCGGCT 2441
 QY 355 GAGCACTTGGCGCGGAGAGACCCAGCCCGGAGAAAACCTTGGCTCTTGGCTTGGAG 414
 Db 2442 GACGACCTTGGCGCGGAGAGACCCAGCCCGGAGAAAACCTTGGCTCTTGGCTTGGAG 2501
 QY 415 GTGAGCAACGAGACTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTA 474
 Db 2502 GTGAGCAACGAGACTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTA 2561
 QY 475 TGGAGTCCCTCGACCGCTTCTGTTCAGAGAGATTCAGAGAGAGAGAGAGAGAGAG 534
 Db 2562 TGGAGTCCCTCGACCGCTTCTGTTCAGAGAGATTCAGAGAGAGAGAGAGAGAGAG 2621
 QY 535 TCTGATTCCTCGATGATTTCTTCCCAATTAGCCATCTCTTAAACTCTTCTCATTC 594
 Db 2622 TCTGATTCCTCGATGATTTCTTCCCAATTAGCCATCTCTTAAACTCTTCTCATTC 2681
 QY 595 CTGGTTTATTTCTGAACCGGTAGGTGTGTCTCAATATTTCTGTCCCTCTGAGA 654
 Db 2682 CTGGTTTATTTCTGAACCGGTAGGTGTGTCTCAATATTTCTGTCCCTCTGAGA 2741
 QY 655 TCCATATCTAGTCTCAATCGCCGTTTCTCTGACAGAGAGAGAGAGAGAGAGAG 714
 Db 2742 TCCATATCTAGTCTCAATCGCCGTTTCTCTGACAGAGAGAGAGAGAGAGAGAG 2801
 QY 715 CTCTGCTTCAAGGCTTGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 774
 Db 2802 CTCTGCTTCAAGGCTTGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2861
 QY 775 CTGGGAG 834
 Db 2862 CTGGGAG 2921
 QY 835 ATCAGTAGACAGCTGCTGCTTCCATGAACGAGAAAAATATAATCATGTTTCTTAA 891
 Db 2922 ATCAGTAGACAGCTGCTGCTTCCATGAACGAGAAAAATATAATCATGTTTCTTAA 2978
 RESULT 8
 AC004195 40878 bp DNA linear PRI 08-DEC-1998
 LOCUS Homo sapiens clone UMGc:y24c027 from 6p21, complete sequence.
 DEFINITION AC004195
 AC004195
 VERSION AC004195.1 GI:3980474
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 40878)
 Janczyk, M., Guillaudoux, T., Vu, Q., Kutayavin, T., Harter, H. and
 Geraghty, D.E.
 Large scale sequence analysis of the human MHC class I region
 Unpublished (1998)
 TITLE JOURNAL
 JOURNAL Fred Hutchinson Cancer Research Center
 The Clinical Research Division
 1100 Fairview Ave. N., P.O. Box 19024
 Seattle, WA 98109-1024
 Contact: Daniel E. Geraghty (geraghty@fhcrc.org)
 2 (bases 1 to 40878)
 Geraghty, D.E. and Olson, M.V.
 Direct Submission
 Submitted (23-FEB-1998) Human Genome Center, University of
 Washington, Box 352145, Seattle, WA 98195, USA
 3 (bases 1 to 40878)
 Geraghty, D.E. and Olson, M.V.
 Direct Submission
 Submitted (08-DEC-1998) Human Genome Center, University of
 Washington, Box 352145, Seattle, WA 98195, USA
 REMARK University of Washington Human Genome Center

COMMENT
 Box 352145 Seattle, WA 98195
 Contact: Daniel E. Geraghty (geraghty@fhcrc.org)
 Dec 8, 1998 this sequence version replaced gi:2905865.
 Overlapping Sequences:
 5' : UMGc:y14c057 (Genbank Accession: AC006047)
 3' : UMGc:y24c203

Sequence Quality Assessment:
 This entry has been annotated with sequence quality
 estimates computed by the Phrap assembly program.
 All manually edited bases have been reduced to quality zero.
 Quality levels above 40 are expected to have less than
 1 error in 10,000 bp.
 Base-by-base quality values are not generally visible from the
 Genbank flat file format but are available as part
 of this entry's ASN.1 file.

Double stranded (DS) coverage: 77.6%
 DS or two chemistry coverage: 100.0%
 Single stranded regions: 0

Sequence Validation:
 This sequence has been validated by Multiple Complete Digest
 Mapping. Comparison of the experimentally derived map digest
 fragments with sequence-predicted fragments is given below.
 Small fragments below a variable cutoff (approximately 400-600bp)
 are not mapped and hence do not appear in the table. There are no
 significant remaining discrepancies between the experimental and
 predicted values. Uniquely ordered fragment groups are separated
 by dashed lines.

Map	Seq	Map	Seq	Map	Seq
BglII	HindIII	NsiI			
5056.53	5005.00	979.90	957.00	8811.76	8685.00
2289.48	2257.00	3644.92	3580.00	9333.67	9154.00
5302.18	5207.00	5611.48	5525.00	814.06	801.00
894.03	880.00	4618.79	4525.00	10116.87	9663.00
3041.57	2999.00	1532.79	1530.00	2432.75	2413.00
14697.70	14691.00	1726.25	1724.00		
		1479.40	1473.00		
		909.61	880.00		
		8223.42	7996.00		
		2404.83	2380.00		
		7342.43	7194.00		

FEATURES
 source
 1. 40878
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6p21"
 /clone="CGM1:A194D6"
 /sub_clone="UMGC:y24c027"
 /cell_line="CGM1"
 /clone_lib="Wash U YAC Library"
 /complement(4237..4519)
 /rpt_family="Alu"
 /complement(4643..5052)
 /rpt_family="Alu"
 /rpt_family="MIR"
 5090..5149
 9346..9586
 repeat_region
 repeat_region
 repeat_region
 repeat_region

ORIGIN

115 AGAGGCACTCAGGCAAGAGGGGCCACCCCTCTCAACCCAGACCCGAGAGGACCCGAGAGGAG 174

Db 27805 ATCAGTAGACAGCTGCTGCTTCATGAAACGAAAAATATAAAATCATGTTTCTTAA 27861

FEATURES

ORIGIN

Db 2411 CTGGGGGAGGCGTACGCTACTGTTCCTTCCTCCACCTGTGGCGGCGGAGAACT 2470
OY 835 ATCAGTAGACAGCTGCTGCTTCATGAAACGGAATAATATCATGTTTCTTAA 891
Db 2471 ATCAGTAGACAGCTGCTGCTTCATGAAACGGAATAATATCATGTTTCTTAA 2527

RESULT 11
AB088114/c
LOCUS 30911 bp DNA linear PRI 08-JAN-2003
DEFINITION Homo sapiens STG, S, SPRI, SEEK1 genes.
ACCESSION AB088114
VERSION AB088114.1 GI:27544424
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1
AUTHORS Shihina,T., Ota,M., Katsuyama,Y., Hashimoto,N. and Inoko,H.
TITLE Genome diversity in HLA: A new strategy for detection of genetic polymorphisms in expressed genes within the HLA class III and class I regions
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 30911)
AUTHORS Shihina,T.
TITLE Direct Submission
JOURNAL Submitted (08-JUL-2002) Takashi Shihina, Tokai University School of Medicine, Molecular Life Science 2, Bohseidai, Isehara, Kanagawa 259-1193, Japan (E-mail:tehiina@is.lcc.u-tokai.ac.jp, Tel:81-463-93-1121, Fax:81-463-94-8884)

FEATURES
source location/Qualifiers
1.30911
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.31"
/cell_line="LTK3"
/cell_type="B cell"
1317..2383
/number=2
complement(join(1473..2383,2581..2647))
/gene="STG"
complement(join(1473..2383,2581..2647))
/gene="STG"
/codon_start=1
/product="hypothetical protein"
/protein_id="BAC54947.1"
/db_xref="GI:27544425"
/translation="MGRVAGSCAPLGLLVCLHPLPARSTGVREKYSQNLGTVL PQLQPSSTGSSNSHPQALDPRNSDLARPLCLVPSADGPPAGGSAVORPSPW GLPAMDWPEDPQWQMAAAEDRLALPEELSYLSAALAGSGPLRESPDPT GLSPKSLILHODSESRLLPRSNLSIAGAGKLIISQRPWSLIHRVLPDHPMTLINSVWG GGGPGTGMGTRPMPHPHPEGIWIQINNOPGMSWGININIRYGGSGWGININ RYGGSGWGINILHYGINNPPPGVLRPPGSSWNIPAFPPPPRLQMG"
2581..2647
/number=1
4938..4983
/number=1
5185..7618
/number=2
complement(join(6114..7618,10423..10459))
/gene="S"
complement(join(6114..7618,10423..10459))
/gene="S"
/codon_start=1
/product="modified desmosin expressed in non-cornified epidermis"
/protein_id="BAC54948.1"
/db_xref="GI:27544426"
/translation="MMALLLAGLLPGLAKSIGTFSDPCKPRTIRINSPNDPCLTQKG DSGGFSYSSSSSSSSISSARSSGSGSSGSSSIAQGSAGSFRGTYGVSVYS

SGSGSLQAAGSSQLGSSSSSHSGSSGSSSSSSSHSSSFQFSSSSPQVNGSAL
PTMDSRYGILNPSQGGSSSSQTSQGVSSGQSVSNORPCSSDIPDPCSGPIVS
HSQPIYPSHSVSGQRPVVVVVDGSGAPGVQPCSNGLPKPCPITPVKS
YGGYEVNGSSDSYLVPMGTYSKGIYPGYFKEKPVGSGPVPFAGPPISEKY
FSSNPILPQSSASNAIAFOVCTGTGVLQCGGTSKPCPSSSSRVBSISSSS
GSPYHPGCSASQSPCPGIGTGFSSSSSSQSGKTILOPCGSSSSSGHPCMSVSLT
LTGGPDGSPHPIDPSAGAKPCGSSSAGKIPCRSIRDLIAOVKPLGQLADEVLPOGE
LIDSPP"
10423..10521
/number=1
15765..15928
/number=2
19676..19752
/number=3
27641..28413
/number=2
complement(join(28058..28413,29079..29133))
/gene="SPRI"
complement(join(28058..28413,29079..29133))
/gene="SPRI"
/codon_start=1
/product="hypothetical protein"
/protein_id="BAC54949.1"
/db_xref="GI:27544427"
/translation="MTLNWKLGLIVLCIHTRGISGSEGHPSHPAEDREAGSPILP
QGPVDPGPPWAPPLFEDPPTPRSPRPMMDLLETGVWPEPEPRTDPPQPPRDPWP
AGPQPPENPWPAPAEVDNRPQSEPDIDPREXRV"
28537..28566
/number=4
28763..28886
/number=5
join(28864..28886,29748..30039)
/gene="SEEK1"
join(28864..28886,29748..30039)
/gene="SEEK1"
/codon_start=1
/product="hypothetical protein"
/protein_id="BAC54950.1"
/db_xref="GI:27544428"
/translation="MEPANHFHMAEDLQAMISKEPHLAATODDCRGRQEDIVSS
HPELFASVLEMAPEEARLQPPPLPPSGIHLASRTILPVLITYSPSHSPFGIJS
LI"
29079..29448
/gene="SEEK1"
/number=1
29748..30167
/number=6

ORIGIN
Query Match 86.8%; Score 773.8; DB 9; Length 30911;
Best Local Similarity 99.7%; Pred. No. 9.5e-166;
Matches 775; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
exon
exon
CDS

Db 115 AGAGGATCTCAAGCAGCGAGGCGCAACCTCTTACCCACCCGAGAGACGAGAGAG 174
Db 28417 ACAGGATCTCAAGCAGCGAGGCGCAACCTCTTACCCACCCGAGAGACGAGAGAG 28358
OY 175 GAGAGCTCCCAACATTGCTCAAGGGCCCCCAAGTCCCGGTACCTTGGCCAGGGGCA 224
Db 28357 GAGAGCTCCCAACATTGCTCAAGGGCCCCCAAGTCCCGGTACCTTGGCCAGGGGCA 28298
OY 235 CCCCCTCTTTAAAGATCTCTCCGCTACCGGCCCCAGTGTGCTCGGAGAGACTGGCT 294
Db 28297 CCCCCTCTTTAAAGATCTCTCCGCTACCGGCCCCAGTGTGCTCGGAGAGACTGGCT 28238
OY 295 GAAACTGAGTGTGCCCCCTGAGACCGCTAGAACGATCTCTCAACTCCCGGCT 354
Db 28237 GAAACTGAGTGTGCCCCCTGAGACCGCTAGAACGATCTCTCAACTCCCGGCT 28178
OY 355 GACGACCTTTGGCCGCGAGAGACCCGAGCCCGGAGAAAACCTTGCGCTCTGCCCCCTGAG 414
Db 28177 GACGACCTTTGGCCGCGAGAGACCCGAGCCCGGAGAAAACCTTGCGCTCTGCCCCCTGAG 28118

```

QY 415 GTGACAAACCGACCTCAGAGAGACCAAGCTAGAACCCCGGGAAGAGTACAGATA 474
DB 28117 GTGACAAACCGACCTCAGAGAGAGACCAAGCTAGAACCCCGGGAAGAGTACAGATA 28058
QY 475 TGGAGTCCCTCAGCCGCTTCTGTTCCAGAGCATCTCCAGGAGACCGAGCCCTCTCCACC 534
DB 28057 TGGAGTCCCTCAGCCGCTTCTGTTCCAGAGCATCTCCAGGAGACCGAGCCCTCTCCACC 27998
QY 535 TCTGATTCCTCCGGAATCTCTCCCAATTAGCTATCTCCCTTAACCTCTCTCATTC 594
DB 27997 TCTGATTCCTCCGGAATCTCTCCCAATTAGCTATCTCCCTTAACCTCTCTCATTC 27938
QY 595 CTCGGTTTATCTGAAACCGGTAAAGTGCTGTCATATTTCTGTCCTGTCCTGAGA 654
DB 27937 CTCGGTTTATCTGAAACCGGTAAAGTGCTGTCATATTTCTGTCCTGTCCTGAGA 27878
QY 655 TCCATCTTACTCTCATATGCCCCGTTTTTCTCTGACAGCTTAAGCTTACTCTCTA 714
DB 27877 TCCATCTTACTCTCATATGCCCCGTTTTTCTCTGACAGCTTAAGCTTACTCTCTA 27818
QY 715 CCTGCGCTCCAGGCTCGGAGCCCACTACCTCCAGCCGCTCTGCGCCGCGAGATCG 774
DB 27817 CCTGCGCTCCAGGCTCGGAGCCCACTACCTCCAGCCGCTCTGCGCCGCGAGATCG 27758
QY 775 CTGCGGAGAGGCTATGCTACTGTCTCTCTCTGCACTGTGAGCGCGGAGAACT 834
DB 27757 CTGCGGAGAGGCTATGCTACTGTCTCTCTCTGCACTGTGAGCGCGGAGAACT 27698
QY 835 ATCAGTAGACGCTGCTCTCTCTCCATGAAACGGAATAATCAATGTTTCTTAA 891
DB 27697 ATCAGTAGACGCTGCTCTCTCTCCATGAAACGGAATAATCAATGTTTCTTAA 27641

```

```

RESULT 12
LOCUS AB023060 39196 bp DNA linear PRI 20-NOV-1999
DEFINITION Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region,
AB023060
ACCESSION AB023060.1 GI:5672629
VERSION HTG.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (sites)
AUTHORS Shihina,T., Tamiya,G., Oka,A., Takishima,N., Yamagata,T.,
Kikkawa,E., Iwata,K., Tomizawa,M., Okuaki,N., Kuwano,Y.,
Watanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,
Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,
Bahrani,S. and Inoko,H.
Molecular dynamics of MHC genesis unraveled by sequence analysis of
the 1,796,938-bp HLA class I region
Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)
2002/5/39
JOURNAL MEDLINE
PUBMED 10557312
2 (bases 1 to 39196)
AUTHORS Shihina,T. and Takishima,N.
TITLE Direct Submission
JOURNAL Submitted (29-JUN-1999) Takashi Shihina, Tokai University School of
Medicine, Department of Molecular Life Science 2, Bohseidai,
Isehara, Kanagawa 259-1193, Japan
(E-mail: tshihina@is.tokai.ac.jp, Tel: 81-463-93-1121,
Fax: 81-463-94-8884)

```

FEATURES

```

source
1..39196
location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
/clone="TY1C2"
/cell_line="BOLETH"

```

```

ORIGIN /issue_type="B cell line"

```

```

Query Match 86.8%; Score 773.8; DB 9; Length 39196;
Best Local Similarity 99.7%; Pred. No. 9.3e-166;
Matches 775; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 115 AGAGGACATCTCAGAGCAGAGGAGCCACCCCTCTACCCACCCGACAGAGACGAGAG 174
DB 10631 ACAGGACATCTCAGAGCAGAGGAGCCACCCCTCTACCCACCCGACAGAGACGAGAG 10690
QY 175 GCAAGCTCCCAACATTGCTCTCAGAGGCCCCCAGTCCCGGTGACCTTGGCCAGAGGCA 234
DB 10691 GCAAGCTCCCAACATTGCTCTCAGAGGCCCCCAGTCCCGGTGACCTTGGCCAGAGGCA 10750
QY 235 CCCCCTCTCTTAAAGATCTCTCGGCTACCCGCGCCAGTGTCTCCGAGAGACCTGGCT 294
DB 10751 CCCCCTCTCTTAAAGATCTCTCGGCTACCCGCGCCAGTGTCTCCGAGAGACCTGGCT 10810
QY 295 GAAACTGAGTCTGAGCCCTCGAACCGCTGAGAACGAGATCTCTCAACTCCCGGCT 354
DB 10811 GAAACTGAGTCTGAGCCCTCGAACCGCTGAGAACGAGATCTCTCAACTCCCGGCT 10870
QY 355 GACGACCTTTGCGCGGAGAGACCCAGCCCTCCAGAAAACCTTGGCTCTGCTGAG 414
DB 10871 GACGACCTTTGCGCGGAGAGACCCAGCCCTCCAGAAAACCTTGGCTCTGCTGAG 10930
QY 415 GTGACAAACCGACCTCAGAGAGAGAGACCTAGACCCCGGGAAGAGTACAGATA 474
DB 10931 GTGACAAACCGACCTCAGAGAGAGAGACCTAGACCCCGGGAAGAGTACAGATA 10990
QY 475 TGGAGTCCCTCAGCCGCTTCTGTTCCAGAGCATCTCCAGACCAACGCGCTCTCAGCC 534
DB 10991 TGGAGTCCCTCAGCCGCTTCTGTTCCAGAGCATCTCCAGACCAACGCGCTCTCAGCC 11050
QY 535 TCTGATTCCTCCGGAATCTCTCCCAATTAGCTATCTCTTAACTCTTCTCATTC 594
DB 11051 TCTGATTCCTCCGGAATCTCTCCCAATTAGCTATCTCTTAACTCTTCTCATTC 11110
QY 595 CTGCGTTTATCTGAAACCGGTAAAGTGCTCTCAATATTTCTGTCCTGCGCTCGAGA 654
DB 11111 CTGCGTTTATCTGAAACCGGTAAAGTGCTCTCAATATTTCTGTCCTGCGCTCGAGA 11170
QY 655 TCCATCTTACTCTCATATGCCCCGTTTTTCTCTGACAGCTTAAGCTTACTCTCTA 714
DB 11171 TCCATCTTACTCTCATATGCCCCGTTTTTCTCTGACAGCTTAAGCTTACTCTCTA 11230
QY 715 CTTGCGCTCCAGGCTCTGAGCCCACTACCTCCAGCCGCTTCTGTCCTGCGCGAGATCG 774
DB 11231 CTTGCGCTCCAGGCTCTGAGCCCACTACCTCCAGCCGCTTCTGTCCTGCGCGAGATCG 11290
QY 775 CTGCGGAGAGGCTATGCTACTGTCTCTCTGCACTGTGAGCGCGGAGAACT 834
DB 11291 CTGCGGAGAGGCTATGCTACTGTCTCTCTGCACTGTGAGCGCGGAGAACT 11350
QY 835 ATCAGTAGACGCTGCTCTCTCTCCATGAAACGGAATAATCAATGTTTCTTAA 891
DB 11351 ATCAGTAGACGCTGCTCTCTCTCCATGAAACGGAATAATCAATGTTTCTTAA 11407

```

```

RESULT 13
LOCUS AL662867/c 70288 bp DNA linear PRI 24-APR-2002
DEFINITION Human DNA sequence from clone Xbae-34D1 on chromosome 6, complete
sequence.
ACCESSION AL662867
VERSION AL662867.5 GI:20068664
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

AUTHORS
TITLE
JOURNAL

COMMENT

Sycamore, N.
Direct Submission
Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonequest@sanger.ac.uk
On Apr 7, 2002 this sequence version replaced g1:19309560.
During difference assembly data is compared from overlapping clones.
Where difference assemblies are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em, EMBL; Sw,
SWISSPROT; Tr, TrEMBL; Wp, WormPeP; Information on the WormPeP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep-xxbac-34d1-is
from a CHORI-502 human bac - COX cell line library VECTOR:
PTABAC2.1
This sequence was generated from part of bacterial clone contigs
constructed by the MHC HaploType Consortium and collaborators.
Further information can be found at
http://www.sanger.ac.uk/HGP/Chr/HMC.
Location/Qualifiers
1. 70288
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/clone="XXbac-34D1"
/clone_1fb="CHORI-502"

FEATURES

source

ORIGIN

Query Match 86.8%; Score 773.8; DB 9; Length 70288;
Best Local Similarity 99.7%; Pred. No. 8.9e-166;
Matches 775; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 115 AGAGGATTCAGGACGAGGAGGACCCCTCTACACCCGAGAGAGACCGAGAGAG 174
Db 67726 ACAGGATTCAGGACGAGGAGGACCCCTCTACACCCGAGAGAGACCGAGAGAG 67667
QY 175 GCAAGGATTCAGGACGAGGAGGACCCCTCTACACCCGAGAGAGACCGAGAGAG 234
Db 67666 GCAAGGATTCAGGACGAGGAGGACCCCTCTACACCCGAGAGAGACCGAGAGAG 67607
QY 235 CCCCCTCTTTGAAGATCTCCGCTACACCCGAGAGAGACCGAGAGAGACCGAGAGAG 294
Db 67606 CCCCCTCTTTGAAGATCTCCGCTACACCCGAGAGAGACCGAGAGAGACCGAGAGAG 67547
QY 295 GAAAGTGAAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 354
Db 67546 GAAAGTGAAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 67487
QY 355 GAGGACCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 414
Db 67486 GAGGACCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 67427
QY 415 GTGAGACACGAGCTCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 474
Db 67426 GTGAGACACGAGCTCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 67367
QY 475 TGAAGTCCCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 534
Db 67366 TGAAGTCCCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 67307
QY 535 TGTGATTCCTCCGAGATTCCTCCCAATTATAGCTATCTCTTAACCTCTTCTCATTTCC 594

Db 67306 TGTGATTCCTCCGAGATTCCTCCCAATTATAGCTATCTCTTAACCTCTTCTCATTTCC 67247
QY 595 CTGGATTTATTTCTGAACCCGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 654
Db 67246 CTGGATTTATTTCTGAACCCGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 67187
QY 655 TCCATATTAATGCTCTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 714
Db 67186 TCCATATTAATGCTCTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 67127
QY 715 CTTGCTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 774
Db 67126 CTTGCTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 67067
QY 775 CTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 834
Db 67066 CTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 67007
QY 835 ATCAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 891
Db 67006 ATCAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 66950

RESULT 14
AP000510
LOCUS
DEFINITION
Homo sapiens genomic DNA, chromosome 6p21.3, HLA Class I region,
section 9/20.
ACCESSION
AP000510 BA000025
VERSION
AP000510.2 GI:7380878
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (21-SEP-1999) Mika Hirakawa, Japan Science and Technology
Corporation (JST), Advanced Databases Department, 5-3, Yonbancho,
Chiyoda-ku, Tokyo 102-0081, Japan [E-mail:mika@tokyo.jst.go.jp,
URL:http://www-alls.tokyo.jst.go.jp/, Tel:81-3-5214-8491,
Fax:81-3-5214-8470]
On Mar 31, 2000 this sequence version replaced g1:5926697.
This sequence is conducted by Tokai University as a JST sequencing
Team.
Principal Investigator: Hidetoshi Inoko Ph.D
Phone:+81-463-93-1121, Fax:+81-463-94-8884,
The sequence is submitted by Human Genome Sequencing in ALLS
project of JST
Japan Science and Technology Corporation (JST)
5-3, Yonbancho, Chiyoda-ku, Tokyo, 102-0081 Japan
for further information about this sequences, please visit our
sequence archive web site (http://www-alls.tokyo.jst.go.jp/HGS/top.
html) or send email to webmaster@www-alls.tokyo.jst.go.jp
Sequence updated (28-Mar-2000).

COMMENT

FEATURES

source

1. 99999
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
2016. 2435
/gene="SERK1"
2016. 2435
/gene="SERK1"
/number=6

```
gene complement(join(2144..2435,3297..3319))
/ gene="SEEK1"
CDS complement(join(2144..2435,3297..3319))
/ gene="SEEK1"
/codon_start=1
/protein_id="BAB63314.1"
/db_xref="GI:15277221"
/translation="MEPANHFWHAGDLOAMISKEFHATODCKRGHTODILVPS
HEPELAVLPMAPFEARLQOPQLPPPSGHLASRTLAFTLLYSPPSHSPGLSL
I"
gene join(2735..3104,3770..4542)
/ gene="SPR1"
exon 2735..3104
/ gene="SPR1"
/ number=1
join(3050..3104,3770..4125)
/ gene="SPR1"
/codon_start=1
/protein_id="BAB63315.1"
/db_xref="GI:15277222"
/translation="MILNKKLLGILVLCIHTRGISGSEHPSHPADREBAGSPTLP
OGPYDPMWGPAPLPEDPPTSPSRPMDLPRTGWPPEPPTDPPQPRPDPMF
AGQDPMWMPAPVMDNRQEBPDIDPREBYR"
gene join(3287..3420,3617..3646)
/ gene="SEEK1"
exon 3297..3420
/ gene="SEEK1"
/ number=5
3617..3646
/ gene="SEEK1"
exon 3770..4542
/ gene="SPR1"
/ number=2
12432..16422
/ gene="SEEK1"
exon 12432..12508
/ gene="SEEK1"
/ number=3
16259..16422
/ gene="SEEK1"
/ number=2
21667..27003
/ gene="S"
gene 21667..21765
/ gene="S"
/ number=1
join(21729..21765,24570..26074)
/ gene="S"
/codon_start=1
/protein_id="BAB63316.1"
/db_xref="GI:15277223"
/translation="MMALLAGLLPGLTAKSIGTSPDKDPRTIRINPNDPLTKG
DSGGSYSYSSSSGSSISGARSGGSSGSSSSTOFSSSTQVQNGSLV
SGSSSTQAGSGSOLGSSSSSHSGSSSSSSSTOFSSSTQVQNGSLV
PTNDSYRGLINPQPOQSSSSQTSVSSSGSVSSNORCSSDIPDSQSGAPLS
HSGYIPISSHSVSGQRPVVVVVDHSGAGVQGPCCNGGIPGCPPIISVKS
YSGYEVGSGSDSYLVPMYTSKGIYPVGYFTKENVKSGPVPSPAAAPRISGKY
FSSNPILPQSOASASAIAPQVGVOLGGGSGKSPSSSSSSSSSSSS
SGPYHPCGASQSPCPGPTGSSSSSSSGKTIIPCGSSSSSGHPCMSYSIT
LTGGPDSHPIDPSBAKPCGSSSAGKIPKSTIRDLIAOVKPLGPOLDPEVFLPGE
LDSBP"
exon 24570..27003
/ gene="S"
/ number=2
26711..26940
/ gene="S"
/ note="RH17634; The location is between each flanking site
of PCR primers."
/ db_xref="GDB:4572035"
gene 27205..27250
/ gene="SEEK1"
exon 27205..27250
```

```
ORIGIN
Query Match 86.8%; Score 773.8; DB 9; Length 99999;
Best Local Similarity 99.7%; Pred. No. 8,7e-166;
Matches 775; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
/ gene="SEEK1"
/ number=1
QY 115 AGAGGCACTCAGGACGAGGAGGACCCCTTCACCCACCCGACAGAGACCGAGAGAG 174
DB 3766 ACAGGCACTCAGGACGAGGAGGACCCCTTCACCCACCCGACAGAGACCGAGAGAG 3825
QY 175 GCAAGCTCCCCAATTCCTCAGAGGCCCCCAGTCCCGGATACCTTGCCAGAGGCA 234
DB 3826 GCAAGCTCCCCAATTCCTCAGAGGCCCCCAGTCCCGGATACCTTGCCAGAGGCA 3885
QY 235 CCCCCTCTTTGAAGATCTCTCCGCTACCCGCGCCAGTGTCTCTGAGAGACTGCTT 294
DB 3886 CCCCCTCTTTGAAGATCTCTCCGCTACCCGCGCCAGTGTCTCTGAGAGACTGCTT 3945
QY 295 GAAACTGAGTCTGGCCCCCTGAAACCGCCTGAAAGGATCTCTCAACTCCCGGCTT 354
DB 3946 GAAACTGAGTCTGGCCCCCTGAAACCGCCTGAAAGGATCTCTCAACTCCCGGCTT 4005
QY 355 GACGACCTTGGCCGAGAGACCCCAAGCCCAAGAAACCCCTGAGCTCTGAGCCCTGAG 414
DB 4006 GACGACCTTGGCCGAGAGACCCCAAGCCCAAGAAACCCCTGAGCTCTGAGCCCTGAG 4065
QY 415 GTGACCAACGACCTCAGAGAGAGCCAGACCTTAGACCAACCCGAGAGAGTAGATTA 474
DB 4066 GTGACCAACGACCTCAGAGAGAGCCAGACCTTAGACCAACCCGAGAGAGTAGATTA 4125
QY 475 TGAAGTCCCTCAGCCGTTCTGTTCCAGAGACCTCAGAGACCCAGCCCTTCACCC 534
DB 4126 TGAAGTCCCTCAGCCGTTCTGTTCCAGAGACCTCAGAGACCCAGCCCTTCACCC 4185
QY 535 TCTGATTCGCCGTAATCTTCCCAATTTAGCTATCTCTTAAACCTTCTCTCAATTC 594
DB 4186 TCTGATTCGCCGTAATCTTCCCAATTTAGCTATCTCTTAAACCTTCTCTCAATTC 4245
QY 595 CTCGCTTTATTTGTAACCCGTAAGGTGTCTCAATATTTCTGTCCCTCCTGAGA 654
DB 4246 CTCGCTTTATTTGTAACCCGTAAGGTGTCTCAATATTTCTGTCCCTCCTGAGA 4305
QY 655 TCCATCTTAGTCTCACAATCGCCGTTTTTTTCTCTGACAGCTTAAGCTTACTCTTA 714
DB 4306 TCCATCTTAGTCTCACAATCGCCGTTTTTTTCTCTGACAGCTTAAGCTTACTCTTA 4365
QY 715 CCTGCGCTTCAGGCTTCGAGCCCACTACCTCCACCCGAGTCTTCTGCGCGGAGTCG 774
DB 4366 CCTGCGCTTCAGGCTTCGAGCCCACTACCTCCACCCGAGTCTTCTGCGCGGAGTCG 4425
QY 775 CTGGGGCAGGGCTATAGTACTGTGTTCCTTCTGCACTGTGTGCGCGGACGAGAACT 834
DB 4426 CTGGGGCAGGGCTATAGTACTGTGTTCCTTCTGCACTGTGTGCGCGGACGAGAACT 4485
QY 835 ATCAGTAGACAGTGTCTGCTTCATGAAACGAAAAAATAATCATGTTTTCTTAA 891
DB 4486 ATCAGTAGACAGTGTCTGCTTCATGAAACGAAAAAATAATCATGTTTTCTTAA 4542
RESULT 15
BX927139/c 135396 bp DNA linear PRI 06-JUN-2004
LOCUS BX927139
DEFINITION Human DNA sequence from clone DANA-72F24 on chromosome 6, complete
sequence.
ACCESSION BX927139
VERSION BX927139.7 GI:48374126
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
```

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (Bases 1 to 135396)
Phillimore, B.
Direct Submission
Submitted (06-JUN-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Jun 6, 2004 this sequence version replaced gi:42734899.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMBEP; Information
on the WORMBEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormbep This sequence

was generated from part of bacterial clone contigs constructed by
the MHC Haplotype Consortium and collaborators. Further information
can be found at
http://www.sanger.ac.uk/HGP/Chr6/MHC
DMA-72F24 is from the DNA-Arts human BAC library MANN.1 VECTOR:
pBelOBAC11.

FEATURES

Source

Location/Qualifiers

1..135396
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/clone="DMA-72F24"
/clone_id="DMA-Arts BAC library MANN.1"

ORIGIN

Query Match 86.8%; Score 773.8; DB 9; Length 135396;
Best Local Similarity 99.7%; Pred. No. 8.5e-166;
Matches 775; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 115 AGAGGATCTCAGGACGAGGACCCCTCTCACCACCCGAGAGAGAGAG 174
DB 129845 ACAGGATCTCAGGACGAGGACCCCTCTCACCACCCGAGAGAGAG 129786
QY 175 GAGAGCTCCCAATGCTCTCAGAGGCCCCCACTCCCGGTGACCTTGGCCAGGGGCA 234
DB 129785 GCAAGGCTCCCAATGCTCTCAGAGGCCCCCACTCCCGGTGACCTTGGCCAGGGGCA 129726
QY 235 CCCCTCTCTTGAAGATCTCCGCTACCCGCCCCAGTGTCTCTGAGAGAGACTGCT 294
DB 129725 CCCCTCTCTTGAAGATCTCCGCTACCCGCCCCAGTGTCTCTGAGAGAGACTGCT 129666
QY 295 GAAACTGAGTGTGCCCCCTGAAACGCTTGAACGAGATCTCTCAACTCCCGGCT 354
DB 129665 GAAACTGAGTGTGCCCCCTGAAACGCTTGAACGAGATCTCTCAACTCCCGGCT 129606
QY 355 GACGACCTTGGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 414
DB 129605 GACGACCTTGGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 129546
QY 415 GTGAGACAGCAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTA 474

DB 129545 GTGAGACAGCAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTA 129486
QY 475 TGAAGTCCCTCAGAGCTTCTGTTCCAGAGATCTCCAGGACCCGCTCTCCACC 534
DB 129485 TGAAGTCCCTCAGAGCTTCTGTTCCAGAGATCTCCAGGACCCGCTCTCCACC 129426
QY 535 TCGATTCCCGGAAATCTCCCAATTAGCCATCTCTTAAACCTTCCCTCATTCG 594
DB 129425 TCGATTCCCGGAAATCTCCCAATTAGCCATCTCTTAAACCTTCCCTCATTCG 129366
QY 595 CTCGGTTTATCTGAACCCGTAAGTGTGTTCTCAATATTTCTGTCCCTCTGAGA 654
DB 129365 CTCGGTTTATCTGAACCCGTAAGTGTGTTCTCAATATTTCTGTCCCTCTGAGA 129306
QY 655 TCCATTAATGCTCTCAGATCCGCTTTTCTCTGAGAGAGCTTAAGCTACTCTTA 714
DB 129305 TCCATTAATGCTCTCAGATCCGCTTTTCTCTGAGAGAGCTTAAGCTACTCTTA 129246
QY 715 CTTGGCTCCAGGCTGAGCCCACTACCTCCACCCGCTTCTGCGCGGCGATCG 774
DB 129245 CTTGGCTCCAGGCTGAGCCCACTACCTCCACCCGCTTCTGCGCGGCGATCG 129186
QY 775 CTGGGAGAGGCTATGCTATGTTCTCTTCTGCACTGTGTGCGCGGAGAGACT 834
DB 129185 CTGGGAGAGGCTATGCTATGTTCTCTTCTGCACTGTGTGCGCGGAGAGACT 129126
QY 835 ATCAGTGAAGCTGCTGCTTCCATGTAACGAGAAATAATCATGTTTCTTAA 891
DB 129125 ATCAGTGAAGCTGCTGCTTCCATGTAACGAGAAATAATCATGTTTCTTAA 129069

Search completed: January 11, 2005, 08:16:02
Job time : 4040 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 11, 2005, 06:51:45 ; Search time 3417 Seconds
(without alignments)
9501.844 Million cell updates/sec

Title: US-09-994-365-1

Perfect score: 891
Sequence: 1 ccccttcggggtcccgagca.....taaaatcatgcttctctaa 891

Scoring table: IDENTITY_NUC
Gapex 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST: *
1: gb esct1: *
2: gb esct2: *
3: gb_hnc: *
4: gb_esct3: *
5: gb_esct4: *
6: gb_esct5: *
7: gb_esct6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	408.2	45.8	419	2	BF513178
C 2	372.2	41.8	634	7	CF764947
C 3	355.2	39.9	593	7	CF765720
C 4	323.8	36.3	336	1	A1150762
C 5	303.6	34.1	383	2	AW315342
C 6	245.8	27.6	422	1	A1596929
C 7	244.2	27.4	562	1	AA530301
C 8	234.8	26.4	451	9	CG484009
C 9	234.4	26.3	466	9	CG484609
C 10	233.4	26.2	419	9	CG484152
C 11	232.4	26.1	243	8	AQ357151
C 12	230.2	25.8	442	9	CG487403
C 13	212.6	23.9	372	8	AO136453
C 14	212.4	23.8	475	9	CG473878
C 15	209.8	23.5	386	9	CG474680
C 16	202.2	22.7	322	9	CG474695
C 17	192	21.5	332	1	AA763309
C 18	179.2	20.1	451	1	AA798896
C 19	169	19.0	395	9	CG528207
C 20	167	18.7	283	9	CG474588
C 21	123.2	13.8	379	1	AA791103
C 22	119.6	13.4	204	1	AA733661
C 23	113.6	12.7	489	8	BH098389
C 24	106	11.9	763	8	AF057073

25	100	11.2	361	1	AA168568
26	86.8	9.7	409	7	CF768607
27	82.4	9.2	494	9	CE197442
28	73.2	8.2	873	9	CL498274
C 29	72.6	8.1	1129	9	AG448563
C 30	68.6	7.7	1236	4	BM927210
C 31	68.4	7.7	1909	9	CL078604
C 32	67.8	7.6	1073	5	BQ961142
C 33	65.6	7.4	1297	5	BQ064843
C 34	65.4	7.3	1703	9	CL078618
C 35	65	7.3	1094	6	CD509997
C 36	64.4	7.2	1153	8	CC252982
C 37	64	7.2	1063	9	CNS040FA
C 38	63.8	7.2	1406	7	CK408425
C 39	63.6	7.1	1365	9	CG745655
C 40	63.2	7.1	1839	9	CG747711
C 41	62.8	7.0	1299	2	BE455157
C 42	62.8	7.0	1351	4	BM922240
C 43	62.2	7.0	1106	6	CD506172
C 44	62.2	7.0	1552	9	CL646265
C 45	62	7.0	920	5	BU929799

ALIGNMENTS

RESULT 1
BF513178/c
LOCUS
DEFINITION
UI-H-BM1-am]-d-04-0-UI-s1 NCI CGAP_Sub7 Homo sapiens cDNA clone
IMAGE:3070111 3', mRNA sequence.
BF513178
BF513178.1 GI:11598357
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/ILMIL at:
www-bio.liln.gov/bdip/image/image.html
Seq primer: M13 Forward
POLYA=yes.
FEATURES
source
1..419
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3070111"
/lab_host="DH10B (Life Technologies)"
/clone_1lb="NCI CGAP Sub7"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; NCI CGAP_Sub7
is a subcloned library derived from NCI CGAP Sub5. The
NCI CGAP Sub7 library had 12 million recombinants. A
single-stranded DNA preparation of NCI CGAP Sub5 was used
as a tracer in a subtractive hybridization with a diver
comprising: the IMAGE pool (NCI CGAP kid3 pool 1 LLM
3334-3337, 3682-3683, 3798-3803 IMAGE Clones
1322376-1323911, 1456008-1456775, 1500552-1502855);
NCI CGAP Kid5 pool 1 LLM 3338-3342, 3722-3725, 3776-3778
(IMAGE Clones 1323912-1325831, 1471368-1472903,

1492104-1493255); NCI CGAP Ins pool 1 LHAM 3575-3582, 3851-3854 (IMAGE Clonoids 1414920-1414991, 1520904-1522439); NCI CGAP G4 pool 1 LHAM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clonoids 1257096-1258631, 1469064-1470983, 147592-1476743); NCI CGAP Pr22 pool 1 LHAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonoids 985608-986759, 1101192-1101959, 1217928-1220615); NCI CGAP Colo pool 1 LHAM 2644-2653, 2871-2872 (IMAGE Clonoids 1057416-1061255, 1144584-1145351). (6% of the driver population), plus a pool of 3,840 arrayed clones from NCI CGAP Sub1 (IMAGE Clonoids 2708616-2710535) and NCI CGAP Sub2 (IMAGE Clonoids 2710536-2712455). (4% of the driver population), plus a pool of 11,136 clones from NCI CGAP Sub3 (IMAGE Clonoids 2712456-2723591) (10% of the driver population), plus a pool of 5,472 clones from NCI CGAP Sub4 (IMAGE Clonoids 2723592-2729326) (40% of the driver population), plus a pool of 4032 clones from NCI CGAP Sub6 (IMAGE Clonoids 2728969-2733190) (40% of the driver population). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806. TAG_TISSUE=ovary TAG_LIB=NCI CGAP_Ov18 TAG_SEQ=GCCACA"]

ORIGIN

Query Match 45.8%; Score 408.2; DB 2; Length 419;
Best Local Similarity 99.3%; Pred. No. 6.4e-91;
Matches 410; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 465 GTACAGATATGAGTCCCTCAGCCGTTCTGTTCAGGAGCATCCAGGACCCAGCC 524
DB 419 GTACAGATATGAGTCCCTCAGCCGTTCTGTTCAGGAGCATCCAGGACCCAGCC 360
QY 525 CTCCTCCACCCCTGATATCCCGTGAATTTCTTCCCAATTTAGCTATCTCTTAACTCT 584
DB 359 CTCCTCCACCCCTGATATCCCGTGAATTTCTTCCCAATTTAGCTATCTCTTAACTCT 300
QY 585 TCCCTCATTCCTCGGTTTATTTCTGAACCCGTAAGTGTCTCAATATTCCTGTC 644
DB 299 TCCCTCATTCCTCGGTTTATTTCTGAACCCGTAAGTGTCTCAATATTCCTGTC 240
QY 645 CTCCTGAGATCCATTAATGATCTCAATGCCCCGTTTCTCTGAGAGCTTAAGCC 704
DB 239 CTCCTGAGATCCATTAATGATCTCAATGCCCCGTTTCTCTGAGAGCTTAAGCC 180
QY 705 TACTCTCTACCTGCGCTCCAGAGGCTGGGCCCACTCTCCACCCGGTCTTCTGCC 764
DB 179 TACTCTCTACCTGCGCTCCAGAGGCTGGGCCCACTCTCCACCCGGTCTTCTGCC 120
QY 765 CGGCGCATTCGCTGGGCGAGGCTATGTAAGTGTCTCTTCTGCGCACTGTGTGGCGGC 824
DB 119 CGGCGCATTCGCTGGGCGAGGCTATGTAAGTGTCTCTTCTGCGCACTGTGTGGCGGC 60
QY 825 GCGCAGACATCATGTAAGAGCTGCTGCTTCCATGAACGAAAAATATAAAA 877
DB 59 GCGCAGACATCATGTAAGAGCTGCTGCTTCCATGAACGAAAAATATAAAA 7

RESULT 2

CF764947

LOCUS

CF764947 634 bp mRNA linear EST 17-OCT-2003

DEFINITION

CF764947 Bos taurus skin cDNA library Bos taurus cDNA clone

ACCESSION

CF764947

VERSION

CF764947.1

KEYWORDS

EST.

SOURCE

Bos taurus (cow)

Bos taurus

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

REFERENCE

Bovinae; Bos.
1 (bases 1 to 634)
Wang, T.H., McWilliam, S. and Lehnert, S.
Transcription Profiling of cattle skin
Unpublished (2003)
Contact: Dr Yonghong Wang
Functional Genomics Lab
CSIRO Livestock Industries
Level 5, Queensland Biosciences Precinct, University of Queensland,
306 Carmody Road St. Lucia QLD Australia
Tel: 07 3214 2445
Fax: 07 3214 2685
Email: Yonghong.Wang@csiro.au
Plate: 40 row: G column: 07.
Location/Qualifiers

FEATURES

1..634
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Hereford Shorthorn"
/db_xref="taxon:9913"
/clone="CCL003088"
/sex="Female"
/issue_type="pooled"
/dev_stage="Adult"
/lab_host="XDL-BlueMRF/strain"
/clone_lib="Bos taurus skin cDNA library"
/note="Organ: skin; Vector: Uni-ZAPXR; Site_1: EcorI;
Site_2: Xho I; Library made from pooled skin of adult
female Hereford-Shorthorn."

ORIGIN

Query Match 41.8%; Score 372.2; DB 7; Length 634;
Best Local Similarity 76.7%; Pred. No. 6.6e-82;
Matches 488; Conservative 0; Mismatches 129; Indels 19; Gaps 2;

QY 56 ACATAGCCATGATCTCTCAACTGGAAGCTCTGGGATCTGTGCTCTTGTCTCTGACACCA 115
DB 2 AGATAGTTAAGATGCTCACTGGAAGCTCTGAGGATCTGTGCTCTTGTCTCTGACACCA 61
QY 116 GAGGCACTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 175
DB 62 GAGGCACTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 121
QY 176 CAGGCTCCCCCAATGCTCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 235
DB 122 AGGAGGCTCCACATTTGCTCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 181
QY 236 CCGCTCTTTTGAAGATCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 295
DB 182 CCGCTCTTTTGAAGATCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 241
QY 296 AAATGGAATCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 355
DB 242 AAATGGAATCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 301
QY 356 ACGACCTTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 415
DB 302 ACGACCTTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 361
QY 416 TGGACACGAGATCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 475
DB 362 TGGACACGAGATCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 421
QY 476 GGAATCCCTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 535
DB 422 GGAATCCCTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 472
QY 536 CTGATTCCTCCGTAATTTCTCCATTTAGCTATGCTCTTAACTCTTCTCTCTCTCTCTCTCTCT 595
DB 473 CTGATTCCTCCGTAATTTCTCCATTTAGCTATGCTCTTAACTCTTCTCTCTCTCTCTCTCTCT 532
QY 536 TCGGTTTATTTCTGAACCCGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 655

Qy	370	GCAGAGACCCGAGCCCCCAGAGAAAAACCCCTGGGCTCTCTGCCCTGAGGTGAGCAACCCGACT	429
Db	316	GCAGAGACCCGAGCTCCAGAAAAACCCCTGGGCTCTCTGCCCTGAGGTGAGCAACCCGACT	375
Qy	430	CAGAGAGAGCCGACCTGAGACCCACCCCGGAGAGTACAGATATGAGTCCCTCAGC	489
Db	376	CACAGAGAGCCGACCTTGAACCCACCCAGGAGAGATACAGATTAACGAGGCC	435
Qy	490	CGTTCTGTGTCACAGGATCTTCAGGACACCAAGCCCTCTCCACCCCTGATATCCCGCGA	549
Db	436	-----ATCTGAGCTTCTGCTCTCAACACATCTTACCCCTTCGATATCCCTTGA	486
Qy	550	ATCTTCCCAATTAGCCTATCTCTTAAACCTCTTCCATTCCTCGGTTTATTCG	609
Db	487	ATTCTCCCAATTATGCTTAATCTTATTCCTTCTCTATTCCTTCAGTTTATTCG	546
Qy	610	AACCCGTGAGGTGTGTTCTCAATATTTCTGTCCCTCCCTGAGATCCATCTTA	664
Db	547	AA-----GATTTTGTGACATATTTTCTGTCCCTCTTGAATGCAATTTA	591
RESULT 4			
LOCUS	A1150762/c		
DEFINITION	A1150762	336 bp	mRNA
VERSION	gc0604.x1 Soares fetal heart Nbh19w		linear
KEYWORDS	IMAGE:1708830 3', mRNA sequence.		EST 30-SEP-1998
ACCESSION	A1150762		
VERSION	A1150762.1	GI:3679231	
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
COMMENT	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheraia; Primates; Carnivora; Homnidae; Homo.		
TITLE	1 (base 1 to 336)		
JOURNAL	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.		
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
FEATURES	Tumor Gene Index		
Source	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-remail.nih.gov		
	This clone is available royalty-free through LNL ; contact the		
	IMAGE Consortium (info@image.llnl.gov) for further information.		
	Seq primer: -40ml3 fwd. EF from Amersham		
	High quality sequence stop: 315.		
	Location/Qualifiers		
	1..336		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:1708830"		
	/sex="unknown"		
	/dev_stage="19 weeks"		
	/lab_host="DH10B (ampicillin resistant)"		
	/clone_id="Soares fetal heart Nbh19w"		
	/note="Organ: heart; Vector: pT73D (Pharmacia) with a		
	modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st		
	strand cDNA was primed with a Not I - oligo(dT) primer [5'		
	TGTTACCAATCTGATGAGGAGCGGCGGCAATCTTTTATTTTATTTT 3']		
	double-stranded cDNA was size selected, ligated to Eco RI		
	adapters (Pharmacia), digested with Not I and cloned into		
	the Not I and Eco RI sites of a modified pT73 vector		
	(Pharmacia). Library went through one round of		
	normalization to a Cot = 5. Library constructed by		
	M.Fatima Bonaldo. This library was constructed from the		
	same fetus as the fetal lung library, Soares fetal lung		
	Nbh19w."		
ORIGIN			
Query Match	36.3%	Score 323.8	DB 1
Best Local Similarity	97.9%	Pred. No. 7.1e-70	
Matches 328	Conservative	0	Mismatches 7
			Indels 0
			Gaps 0

QY	557	CCAAATTGAGCCATCTCCCTTAAACCGTCGTCATTCCTGGGTTTTATTCGAACCGGT	616
Db	336	CCAAATTGAGCCATTTCTTAAACCTTTTCCCTCATTCCTCGGTTTTATTGGAACCGGT	277
QY	617	AAGGTGGTGTTCTCAATATTTCTGTCCCTCCTGAGATCATACTTAAGTCTCTCATATGG	676
Db	276	AAGGTGGTGTTCTCAATATTTCTGTCCCTCCTGAGATCATACTTAAGTCTCTCATATGG	217
QY	677	CCCGTTTTTTCCTGACAGCCTAAGACCTACCTCTGACCTCCAGGCGCTGAGGCC	736
Db	216	CCCGTTTTTTCCTGACAGCCTAAGCTACTCTCTACCTGCGCTCAGGCGCTGAGGCC	157
QY	737	CACCTAAGCTCCCAACCCGGTCTTCTCTGCGCGCGCATTCGTGGGGCAGGGCTATGGTACTG	796
Db	156	CACCTAAGCTCCCAACCCGGTCTTCTCTGCGCGCGCATTCGTGGGGCAGGGCTATGGTACTG	97
QY	797	TGTTCCCTTCTGCGCACTGCTGCGCGCGGGCAGAACTATCAGTAGACAGCTGCTGCTTC	856
Db	96	TGTTCCCTTCTGCGCACTGCTGCGCGGGGAGAACTATCAGTAGACAGCTGCTGCTTC	37
QY	857	CATGAAACGGAATAAATAATCATGTTTTCTTAA	891
Db	36	CATGAAACGGAATAAATAATCATGTTTTCTTAA	2

RESULT 5			
AMJ15342			
LOCUS	383 bp	linear	EST 09-JUL-2000
DEFINITION	12593 MARC 2Pig Sus scrofa cDNA 5'	mRNA sequence.	
ACCESSION	AMJ15342		
VERSION	AMJ15342.1	GI:6744598	
KEYWORDS	EST,		
SOURCE	Sus scrofa (pig)		

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	COMMENT
1 (bases 1 to 383)	Mammalia; Euthera; Cetartiodactyla; Suidae; Suidae; Sus.				
	Fehrenkamp, S.C., Smith, T.P.L., Frelking, B.A., Cho, J., White, J.,				
	Vallier, J., Wise, T., Rohrer, G.A., Pettee, G., Sultana, R.,				
	Quackenbush, J., and Keele, J.W.				
	Porcine gene discovery by normalized cDNA-library sequencing and				
	EST cluster assembly				
	Mamm. Genome 13 (8), 475-478 (2002)				
	22213789				
	12226715				
	Contact: Smith TPL				

Email: smuth@emmail.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -m5score 20
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCAACGACG
Plate: 8 row: A column: 14
Seq primer: ATTAGGTGACACCTAATG.
Location/Qualifiers
1..383
source

```

/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="Pooled"
/lab_host="DH10B"
/clone_lib="MARC 2Pig"
/note="Vector: pCMV SPOR6; Site 1: NotI; Site 2: SalI
library made from pooled tissue from testis ovary,
endometrium, hypothalamus, pituitary, and placenta."

```

Query Match 34.1%; Score 303.6; DB 2; Length 383;

	Best Local Similarity	87.2%	Pred. No. 7,9e-65	
	Matches	333;	Conservative	0; Mismatches 49; Indels 0; Gaps 0
QY	75	CTGAAGCTCCTGGGGAATCTGGTCTTTTGCTGTACACCAAGGCATCTGAGCAGCGA	134	
Db	2	CTGAAGCTACTGGGGAATCTGGTCTTTTGCTGTTCGCCGAGGCATCTCAGGAGCGG	61	
QY	135	GGGCGACCCCTCTCAACCCACGAGAGACCGAGAGAGCGCTCCCAATTGCC	194	
Db	62	AAACCAACCATCTCCGCCATCCACGAGAGCCCTCAGAGAGAGAGGCTCCCAACATTGCC	121	
QY	195	TCAGGAGCCCCCAGTCCCGGATGACCTCTGGCCAGGGGCAACCCCTCTTTGGAATCC	254	
Db	122	TGGGGGGCCCCCAATCCCGGATGACCTTGGCCAGGGGTACTCTTATCTTTGAGAGAC	181	
QY	255	TCGCGCTTACCCGCCCCAGTGTCTCCCTGAGAGACCTGTCTGAAACTGAGACTTGAGCCCC	314	
Db	182	TCAGACTCGAAGGGGCCAATCGTCTCCCTGAGAGACCTGTCTGAATCTGAGACTTGAGCCCC	241	
QY	315	TGAACCGCTTGAAACGATCTCTCTCAACCTTCCCGAGCTGACGACCCCTTGAGCGGACG	374	
Db	242	TGAACCCCTCTGATCTGATCTCCCTCAACCTCCCGGCTGACGACCCCTTGAGCGGACG	301	
QY	375	AACCCAGCCCCCAGAAAAACCCCTGGCTCTCTGCCCCCTGAGGTGACCAACGACTTCAGGA	434	
Db	302	AACCCAGCTTCAGAAAAACCCCTGGCCACCTGCCCCCTGAGGTGACCAACGATCCAGGA	361	
QY	435	GGAGCAGACTTGAACCCACCC	456	
Db	362	GGAGCAGACTTGAACCCACCC	383	

	RESULT	6							
	LOCUS	A1596929							
	DEFINITION	A1596929	422 bp	mRNA	linear	EST 21-APR-1999			
	ACCESSION	VJ6611.Y1	Stratagene mouse ekin	(#37313)	Mus musculus cDNA clone				
	VERSION	IMAGE:932108_5,	mRNA sequence.						
	KEYWORDS	A1596929..1	GI:4605977						
	SOURCE	Est.							
	ORGANISM	Mus musculus (house mouse)							
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Bases 1 to 422) Marra,M., Hallier,D., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,W., Pape,D., Harvey,N., Schurk,R., Altner,E., Korn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.. The WashU-NCI Mouse EST Project 1999 Contact: Marra M/WashU-NCI Mouse EST Project 1999 Unpublished (1999)							
TITLE	JOURNAL								
COMMENT									

Email: mouseest@atson.wustl.edu
This clone is available royalty-free through IML; contact the
IMAGE Consortium (info@image.jml.gov) for further information.
MGI:537028
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
correct orientation)
Seq primer: -40RP from Gibco
High quality sequence stop: 396.
Location/Qualifiers
1..422

```
FEATURES
source
location/qualifiers
1..422
/organism="Mus musculus"
/mol_type="mRNA"
/Strain="C57BL/6"
/dd_xref="taxon:10090"
/clone="IMAGE:932108"
```

```

/sax="females"
/tissue type="whole skin"
/dev stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_id="Stratagene mouse skin (#937313)"
/notes="Organ: skin; Vector: pBluescript SK-; Site: 1:
EcORI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector: -5'
adaptor sequence: 5' GAATTCGCGACGAG 3'-3' adaptor
sequence: 5' CTCGAGTTTCTTTTCTTTT 3'"

```

ORIGIN

```

Query Match      27.6%; Score 245.8; DB 1; Length 422;
Best Local Similarity 79.2%; Pred. No. 2.1e-50;
Matches 305; Conservative 0; Mismatches 77; Indels 3; Gaps 1;

QY 94 CTGGTCTTTGCTGTCACACCAAGGATCTTCAGGCGAGGCGACCCCTTCACCCA 153
DB 2 CTGGTCTTTGCTGTCAGAGGATTTCAAGCA--ATGGCGACCTTCTCCGGA 58
QY 154 CCGCGAAGAGCCGAGAGGAGGAGGCTCCCAATTGCTCAGGCGCCCGGAGTCCCC 213
DB 59 TCTACAGACACCCAGAGAGAGAGAGTCCCACTTGCCTCTGGAACCCCAATCCT 118
QY 214 GGTGACCTTTGGCCAGGAGGAGACCCCTCTCTTTGAAGATCTCGGCGCTACCGCCAGT 273
DB 119 GGTATCTCTGCGCTGCGGCGCTCTCTTTGTTATGAACTTCGCTCCAGGCTCCAC 178
QY 274 GGTGACCTTTGGCCAGGAGGAGACCCCTCTCTTTGAAGATCTCGGCGCTACCGCCAGT 333
DB 179 GGTGACCTTTGGCCAGGAGGAGACCCCTCTCTTTGTTATGAACTTCGCTCCAGGCTCCAC 238
QY 334 CTGCTCTCAACTCCCGGCTCTGAGAGCCCTTGGCGGAGAGACCCCGAGCCCGGAGAAAC 393
DB 239 CCGCTTAACTCTCTGCTGATGAGCCCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 298
QY 394 CCGTGGCTCTGCTGCGGCTGAGAGTGAACCACTGAGAGAGAGAGAGAGAGAGAGAGAG 453
DB 299 CCGTGGCTCTGCTGCGGCTGAGAGTGAACCACTGAGAGAGAGAGAGAGAGAGAGAGAG 358
QY 454 CCGCGGAGAGATACAGATATGGA 478
DB 359 CCGCGGAGAGATATGATAGGGA 383

```

```

RESULT 7      562 bp      mRNA      linear      EST 22-JUL-1997
AA530301      v46e11.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
LOCUS         IMAGE:932108 5', mRNA sequence.
DEFINITION    AA530301
ACCESSION     AA530301.1 GI:2273007
VERSION       EST.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
               Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
               1 (bases 1 to 562)
REFERENCE     Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
AUTHORS       Giesel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
               Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,
               Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
               Waterston, R.
               The WashU-HMI Mouse EST Project
               Unpublished (1996)
               Contact: Marra M/Mouse EST Project
               WashU-HMI Mouse EST Project
               Washington University School of Medicine
               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
               Tel: 314 286 1800
               Fax: 314 286 1810
               Email: mouseest@watson.wustl.edu

```

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MG1:537028

Seq primer: -28m3 rev1 ET from Amersham

High quality sequence stop: 221.

Location/Qualifiers

FEATURES

source

```

1.562
/organism="Mus musculus"
/mol type="mRNA"
/db_xref="taxon:10090"
/db_xref="IMAGE:932108"
/sex="females"
/tissue type="whole skin"
/dev stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_id="Stratagene mouse skin (#937313)"
/notes="Organ: skin; Vector: pBluescript SK-; Site: 1:
EcORI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector: -5'
adaptor sequence: 5' GAATTCGCGACGAG 3'-3' adaptor
sequence: 5' CTCGAGTTTCTTTTCTTTT 3'"

```

ORIGIN

```

Query Match      27.4%; Score 244.2; DB 1; Length 562;
Best Local Similarity 79.0%; Pred. No. 5.6e-50;
Matches 304; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

QY 94 CTGGTCTTTGCTGTCACACCAAGGATCTTCAGGCGAGGCGACCCCTTCACCCA 153
DB 1 CTGGTCTTTGCTGTCAGAGGATTTCAAGCA--ATGGCGACCTTCTCCGGA 57
QY 154 CCGCGAAGAGCCGAGAGGAGGAGGCTCCCAATTGCTCAGGCGCCCGGAGTCCCC 213
DB 58 TCTACAGACACCCAGAGAGAGAGAGTCCCACTTGCCTCTGGAACCCCAATCCT 117
QY 214 GGTGACCTTTGGCCAGGAGGAGACCCCTCTCTTTGAAGATCTCGGCGCTACCGCCAGT 273
DB 118 GGTATCTCTGCGCTGCGGCGCTCTCTTTGTTATGAACTTCGCTCCAGGCTCCAC 177
QY 274 GGTGACCTTTGGCCAGGAGGAGACCCCTCTCTTTGAAGATCTCGGCGCTACCGCCAGT 333
DB 178 GGTGACCTTTGGCCAGGAGGAGACCCCTCTCTTTGTTATGAACTTCGCTCCAGGCTCCAC 237
QY 334 CTGCTCTCAACTCCCGGCTCTGAGAGCCCTTGGCGGAGAGACCCCGAGCCCGGAGAAAC 393
DB 238 CCGCTTAACTCTCTGCTGATGAGCCCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 297
QY 394 CCGTGGCTCTGCTGCGGCTGAGAGTGAACCACTGAGAGAGAGAGAGAGAGAGAGAGAG 453
DB 298 CCGTGGCTCTGCTGCGGCTGAGAGTGAACCACTGAGAGAGAGAGAGAGAGAGAGAGAG 357
QY 454 CCGCGGAGAGATACAGATATGGA 478
DB 358 ACCCGAGAGATATGATAGGGA 382

```

```

RESULT 8      451 bp      DNA      linear      GSS 01-OCT-2003
CG484009      G8T17807 Mus musculus 1295v/Ev Mus musculus genomic clone G8T17807,
LOCUS         genomic survey sequence.
DEFINITION    CG484009
ACCESSION     CG484009.1 GI:37239343
VERSION       GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
               1 (bases 1 to 451)
REFERENCE     Zambrowicz, B.P., Abuln, A., Ramirez-Solis, R., Richter, J.J.,
AUTHORS       Piggett, J., Beltrandeirio, H., Buxton, E.C., Edwards, J., Finch, R.A.,

```


JOURNAL COMMENT
 TITLE
 Unpublished (1997)
 Other GSSs: CITBI-EI-2534014.TR
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES
 SOURCE
 Location/Qualifiers
 1..416
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="129Sv/Bv"
 /db_xref="taxon:10090"
 /clone="OST13885"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129Sv/Bv"

ORIGIN

Query Match 26.2%; Score 233.4; DB 9; Length 416;
 Best Local Similarity 79.3%; Pred. No. 2.6e-47;
 Matches 276; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

131 GCGAGGGGACCCCTCTCACCACCCGAGAGACCCGAGAGAGGAGGAGGCTCCCAACAT 190
 9 GCAATGGGACCTCTTCCGAGATTACAGACCCAGAGAGAGAGAGATCCCAACAT 68
 191 TGCCCTGAGGAGCCCGCACTCCCGGTGACCCCTGGCCAGGGGCAACCCCTCTCTTTGAG 250
 69 TGCCCTGAGGAGCCCGCACTCCCGGTGATCCCTGGCCAGGGGCGCTCTTTGTTGATG 128
 251 ATCTCCGCTTACCCGCGCCCAAGTGTCTCTGAGAGACCTGCTGAAATGAGATCTGGC 310
 129 AACCTCCGCTTCAAGGCTCCCAACCGTCCCTGAGAGATCTTCTGACAGTGTGCTGGC 188
 311 CCCCTGAGCGGCTTGAAGAGATCTCTCAACCTCCCGGCGCTGAGAGACCTTGGCCG 370
 189 CCCCAAGCCCCCAAGCACTATCCCTTAACCTCTGCTGATGATACCTTGGCCAG 248
 371 CAGGAGCCGAGCCCGCAGAAAAACCTTGGCTCTCTGACCTGAGGTGAGCAACGACCTC 430
 249 CAGGAGCCGAGCCCGCAGAAAAACCTTGGCTCTCTGACCTGAGGTGAGCAATGATCTC 308
 431 AGGAGAGCCGAGACCTTGAAGACCCGCGGAGAGATACATATATGGA 478
 309 AGGAGAGCCGAGACCTTGAAGACCCGCGGAGAGATATATGAGGGA 356

RESULT 11
 A0357151/c 243 bp DNA linear GSS 24-JAN-1999
 LOCUS CITBI-EI-2534014.TF CITBI-EI Homo sapiens genomic clone 2534014,
 DEFINITION genomic survey sequence.
 ACCESSION A0357151
 VERSION A0357151 GI:4184324
 KEYWORDS GSS.
 ORGANISM Homo sapiens (human)
 SOURCE Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 243)
 Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and
 Venter, J.C.
 TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
 Map Building

JOURNAL COMMENT

Unpublished (1997)
 Other GSSs: CITBI-EI-2534014.TR
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES SOURCE

Location/Qualifiers
 1..243
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="2534014"
 /sex="male"
 /cell_type="sperm"
 /clone_lib="CITBI-EI"
 /note="Vector: pBelOAC11, Site_1: EcoRI; Site_2: EcoRI;
 Caltech Human BAC Library D"

ORIGIN

Query Match 26.1%; Score 232.4; DB 8; Length 243;
 Best Local Similarity 97.5%; Pred. No. 4.3e-47;
 Matches 236; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

300 TGGAGTGTGGGCCCCCTGTAACCGGCTAGACGATCTCTCAACCTCCCGGCTGAGCA 359
 243 TGGAGTGTGGGCCCCCTGTAACCGGCTAGACGATCTCTCAACCTCCCGGCTGAGCA 184
 360 CCTTGGCCGCGCAGAGACCCAGCCCGCAGAAAAACCCCTGGCTCTCTGAGTGA 419
 183 CCTTGGCCGCGCAGAGACCCAGCCCGCAGAAAAACCCCTGGCTCTCTGAGTGA 124
 420 CAACCGACCTCAGAGAGAGCCAGACCTTGAACCCAGCCCGGAGAGATACATATATGAG 479
 123 CAACCGACCTCAGAGAGAGCCAGACCTTGAACCCAGCCCGGAGAGATACATATATGAG 64
 480 TCCCTCAGCGGCTTCTGTCCAGGACCTTCAGGACCCAGCGGCTCTCCACCTCTGA 539
 63 TCCCTCAGAAATCTGTTCAGGACCTTCAGGACCCAGCGGCTCTCTACCTCTGA 4
 540 TT 541
 3 TT 2

RESULT 12
 CG487403 442 bp DNA linear GSS 01-OCT-2003
 LOCUS OST22893 Mus musculus 129Sv/Bv Mus musculus genomic clone OST22893,
 DEFINITION genomic survey sequence.
 ACCESSION CG487403
 VERSION CG487403 GI:37246315
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 442)
 Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
 Piggott, J., Beltranderio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
 Key, B.W. Jr., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaiang, C.,
 Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
 Spark, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
 Zhu, Q., Person, C. and Sands, A.T.
 TITLE Mxl kinase deficiency lowers blood pressure in mice: a gene-trap

Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 11, 2005, 09:15:10 ; Search time 111 Seconds
(without alignments)
5705.522 Million cell updates/sec

Title: US-09-994-365-1

Perfect score: 891

Sequence: 1 cctcttggtggtcccgagca.....taaaatcatgtttcttaa 891

Scoring table: OLIGO_NNC

Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 355394441 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	9.8	248	US-09-621-976-9776	Sequence 9776, Ap
2	26	2.9	204	US-09-513-999C-27772	Sequence 27772, A
3	20	2.2	229	US-08-639-763-17	Sequence 17, Appl
4	20	2.2	229	US-08-639-763-18	Sequence 18, Appl
5	20	2.2	229	US-09-171-755B-17	Sequence 17, Appl
6	20	2.2	229	US-09-171-755B-18	Sequence 18, Appl
7	20	2.2	1740	US-09-023-655-1110	Sequence 1110, Ap
8	20	2.2	1907	US-08-184-327A-3	Sequence 3, Appl1
9	20	2.2	1907	PCT-US95-00670-3	Sequence 3, Appl1
10	20	2.2	2034	US-08-078-311-15	Sequence 15, Appl
11	20	2.2	2034	US-08-460-402-15	Sequence 15, Appl
12	19	2.1	448	US-09-621-976-8768	Sequence 8768, Ap
13	19	2.1	455	US-09-621-976-8742	Sequence 8742, Ap
14	19	2.1	465	US-09-621-976-8732	Sequence 8732, Ap
15	19	2.1	468	US-09-621-976-8667	Sequence 8667, Ap
16	19	2.1	476	US-09-621-976-8751	Sequence 8751, Ap
17	19	2.1	483	US-09-621-976-8751	Sequence 8751, Ap
18	19	2.1	770	US-09-976-594-597	Sequence 9776, Ap
19	18	2.0	825	US-09-252-991A-4178	Sequence 4178, Ap
20	18	2.0	945	US-09-489-039A-4719	Sequence 4719, Ap
21	18	2.0	984	US-09-252-991A-4635	Sequence 4635, Ap
22	18	2.0	1171	US-08-336-257A-1	Sequence 1, Appl1
23	18	2.0	1171	5386025-1	Patent No. 5386025
24	18	2.0	1258	US-09-016-434-1294	Sequence 1294, Ap
25	18	2.0	1377	US-09-252-991A-4240	Sequence 4240, Ap
26	18	2.0	2094	US-09-252-991A-4535	Sequence 4535, Ap
27	18	2.0	71989	US-09-443-501A-2	Sequence 2, Appl1

C	28	18	2.0	1664976	4	US-08-916-421B-1	Sequence 1, Appl1
C	29	18	2.0	1664976	4	US-09-692-570-1	Sequence 1, Appl1
C	30	17	1.9	108	4	US-09-445-247-17	Sequence 17, Appl1
C	31	17	1.9	222	4	US-09-248-796A-10943	Sequence 10943, A
C	32	17	1.9	449	4	US-09-621-976-8678	Sequence 8678, Ap
C	33	17	1.9	570	4	US-09-016-434-789	Sequence 789, Ap
C	34	17	1.9	1050	1	US-08-180-209B-16	Sequence 16, Appl
C	35	17	1.9	1050	1	US-08-385-745-16	Sequence 16, Appl
C	36	17	1.9	1050	3	US-08-485-388-16	Sequence 16, Appl
C	37	17	1.9	1050	3	US-08-474-853-16	Sequence 16, Appl
C	38	17	1.9	1050	3	US-09-166-205B-16	Sequence 16, Appl
C	39	17	1.9	1050	5	PCT-US94-02629-16	Sequence 16, Appl
C	40	17	1.9	1221	1	US-08-229-287-3	Sequence 3, Appl1
C	41	17	1.9	1449	4	US-09-710-797-23	Sequence 23, Appl
C	42	17	1.9	1509	4	US-09-724-797-89	Sequence 89, Appl
C	43	17	1.9	1636	4	US-09-023-655-1005	Sequence 1005, Ap
C	44	17	1.9	1725	3	US-09-134-001C-2572	Sequence 2572, Ap
C	45	17	1.9	2007	3	US-09-052-089A-7	Sequence 7, Appl1

ALIGNMENTS

```
RESULT 1
US-09-621-976-9776/c
; Sequence 9776, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 9776
; LENGTH: 248
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 188
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-9776

Query Match          9.8%; Score 87; DB 4; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.1e-33;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 293 CTGAAGTCGAGTCTGCGCCCTGAAACCGCTTGAGACGATCTCTCAACCTCCCGGC 352
Db 186 CTGAAGTCGAGTCTGCGCCCTGAAACCGCTTGAGACGATCTCTCAACCTCCCGGC 127

Cy 353 CTGACGACCTTGCGCCGCGAGACCC 379
Db 126 CTGACGACCTTGCGCCGCGAGACCC 100

RESULT 2
US-09-513-999C-27772/c
; Sequence 27772, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
```

PRIOR APPLICATION NUMBER: US 60/122,487
 PRIOR FILING DATE: 1999-02-26
 NUMBER OF SEQ ID NOS: 36681
 SOFTWARE: Patent.pm
 SEQ ID NO 27772
 LENGTH: 204
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-513-999C-27772

Query Match
 Best Local Similarity 2.9%; Score 26; DB 4; Length 204;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 744 CTCACACCCGCTCTCTCCGCGC 769
 DB 26 CTCACACCCGCTCTCTCTCCGCGC 1

RESULT 3
 US-08-639-763-17
 Sequence 17, Application US/08639763
 Patent No. 5712127
 GENERAL INFORMATION:
 APPLICANT: Genescope, Inc.
 TITLE OF INVENTION: SUBSTRUCTIVE AMPLIFICATION
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David J. Weltz, Wilson Sonsini Goodrich & Rosati
 STREET: 650 Page Mill Road
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1050
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch diskette
 OPERATING SYSTEM: IBM compatible
 SOFTWARE: Wordperfect for windows 6.1,
 SOFTWARE: ASCII (DOS) TEXT format
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/639,763
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/639,763
 FILING DATE: 29-APRIL-96
 ATTORNEY/AGENT INFORMATION:
 NAME: David J. Weltz
 REGISTRATION NUMBER: 38,362
 REFERENCE/DOCKET NUMBER: GENE 4001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 493-9300
 TELEFAX: (415) 493-6811
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 229 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-639-763-17

Query Match
 Best Local Similarity 2.2%; Score 20; DB 1; Length 229;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 GCTCCTGGGAGATCTGTC 100
 DB 72 GCTCCTGGGAGATCTGTC 91

RESULT 4
 US-08-639-763-18/c

Sequence 18, Application US/08639763
 Patent No. 5712127
 GENERAL INFORMATION:
 APPLICANT: Genescope, Inc.
 TITLE OF INVENTION: SUBSTRUCTIVE AMPLIFICATION
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David J. Weltz, Wilson Sonsini Goodrich & Rosati
 STREET: 650 Page Mill Road
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1050
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch diskette
 OPERATING SYSTEM: IBM compatible
 SOFTWARE: Wordperfect for windows 6.1,
 SOFTWARE: ASCII (DOS) TEXT format
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/639,763
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/639,763
 FILING DATE: 29-APRIL-96
 ATTORNEY/AGENT INFORMATION:
 NAME: David J. Weltz
 REGISTRATION NUMBER: 38,362
 REFERENCE/DOCKET NUMBER: GENE 4001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 493-9300
 TELEFAX: (415) 493-6811
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 229 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-639-763-18

Query Match
 Best Local Similarity 2.2%; Score 20; DB 1; Length 229;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 GCTCCTGGGAGATCTGTC 100
 DB 158 GCTCCTGGGAGATCTGTC 139

RESULT 5
 US-09-171-755B-17
 Sequence 17, Application US/09171755B
 Patent No. 6498024
 GENERAL INFORMATION:
 APPLICANT: MALEK, Lawrence T.
 APPLICANT: SOONANAN, Roy R.
 TITLE OF INVENTION: SUBSTRUCTIVE AMPLIFICATION KIT USEFUL IN THE DIAGNOSIS OF
 FILE REFERENCE: G01D 0181S
 CURRENT APPLICATION NUMBER: US/09/171,755B
 PRIOR FILING DATE: 1999-03-18
 PRIOR APPLICATION NUMBER: PCT/US97/07253
 PRIOR FILING DATE: 1997-04-29
 PRIOR APPLICATION NUMBER: US 08/639,763
 PRIOR FILING DATE: 1996-04-29
 NUMBER OF SEQ ID NOS: 38
 SOFTWARE: Patent Ver. 2.1
 SEQ ID NO 17
 LENGTH: 229
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-171-755B-17

Query Match 2.2%; Score 20; DB 4; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 GCTCCTGGGATCCTGCTCC 100
Db 72 GCTCCTGGGATCCTGCTCC 91

RESULT 6
US-09-171-755B-18/C
Sequence 18, Application US/09171755B
Patent No. 6498024
GENERAL INFORMATION:
APPLICANT: MALEK, Lawrence T.
APPLICANT: SOOKNANAN, Roy R.
TITLE OF INVENTION: SUBTRACTIVE AMPLIFICATION KIT USEFUL IN THE DIAGNOSIS OF
FILE REFERENCE: GOND-01805
CURRENT APPLICATION NUMBER: US/09/171,755B
CURRENT FILING DATE: 1999-03-18
PCT/US97/07253
PRIOR APPLICATION NUMBER: PCT/US97/07253
PRIOR FILING DATE: 1997-04-29
PRIOR APPLICATION NUMBER: US 08/639,763
PRIOR FILING DATE: 1996-04-29
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 229
TYPE: DNA
ORGANISM: Homo sapiens
US-09-171-755B-18

Query Match 2.2%; Score 20; DB 4; Length 229;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 GCTCCTGGGATCCTGCTCC 100
Db 158 GCTCCTGGGATCCTGCTCC 139

RESULT 7
US-09-023-655-1110
Sequence 1110, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: COCKS, Benjamin G.
APPLICANT: Susan G. Stuart
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SRO ID NO: 1110:
SEQUENCE CHARACTERISTICS:
LENGTH: 1740 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g184262
US-09-023-655-1110

Query Match 2.2%; Score 20; DB 4; Length 1740;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 GCTCCTGGGATCCTGCTCC 100
Db 800 GCTCCTGGGATCCTGCTCC 819

RESULT 8
US-08-184-327A-3
Sequence 3, Application US/08184327A
Patent No. 5498599
GENERAL INFORMATION:
APPLICANT: Choi, Esther S.
APPLICANT: Hokom, Martha M.
APPLICANT: Hunt, Pamela L.
APPLICANT: Nichol, Janet L.
TITLE OF INVENTION: Compositions and Methods for Stimulating
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc., U.S. Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: CA
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,327A
FILING DATE: 20-JAN-1994
CLASSIFICATION: 51A
INFORMATION FOR SRO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1907 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1905
US-08-184-327A-3

Query Match 2.2%; Score 20; DB 1; Length 1907;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 GCTCCTGGGATCCTGCTCC 100

Db 800 GCTCCTGGGGATCCTGTC 819

RESULT 9

PCT-US95-00670-3
Sequence 3, Application PC/TUS9500670
GENERAL INFORMATION:
APPLICANT: Choi, Esther S.
APPLICANT: Hokom, Martha M.
APPLICANT: Hunt, Pamela
APPLICANT: Nichol, Janet L.
TITLE OF INVENTION: Compositions And Methods For Stimulating
TITLE OF INVENTION: Platelet Production
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc., U.S. Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: CA
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00670
FILING DATE: 18-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,327
FILING DATE: 20-JAN-1994
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1907 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1905
PCT-US95-00670-3

Query Match 2.2%; Score 20; DB 5; Length 1907;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 GCTCCTGGGGATCCTGTC 100
Db 800 GCTCCTGGGGATCCTGTC 819

RESULT 10

US-08-078-311-15
Sequence 15, Application US/08078311
Patent No. 5925750
GENERAL INFORMATION:
APPLICANT: Charon, Martine
APPLICANT: Gieselbrecht, Silvie
APPLICANT: Penciolelli, Jean-Francios
APPLICANT: Souyri, Michele
APPLICANT: Tambourin, Pierre
APPLICANT: Varlet, Paule
APPLICANT: Vigon, Isabelle
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
TITLE OF INVENTION: Myeloproliferative Disease
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5925750west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/078,311
FILING DATE: 18-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR90/00762
FILING DATE: 19-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchuk, Katherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 8076.84USWO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2034 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 4..1908
US-08-078-311-15

Query Match 2.2%; Score 20; DB 2; Length 2034;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 GCTCCTGGGGATCCTGTC 100
Db 803 GCTCCTGGGGATCCTGTC 822

RESULT 11

US-08-460-402-15
Sequence 15, Application US/08460402
Patent No. 5989833
GENERAL INFORMATION:
APPLICANT: Charon, Martine
APPLICANT: Gieselbrecht, Silvie
APPLICANT: Penciolelli, Jean-Francios
APPLICANT: Souyri, Michele
APPLICANT: Tambourin, Pierre
APPLICANT: Varlet, Paule
APPLICANT: Vigon, Isabelle
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
TITLE OF INVENTION: Myeloproliferative Disease
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5989833west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,402
FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/309,259
FILING DATE: 20-SEP-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,311
FILING DATE: 18-JUN-1993
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/FR90/00762
FILING DATE: 14-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Randall A. Hillson
REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 8076.84US03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2034 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 4..1908
US-08-460-402-15
```

```
Query Match 2.2%; Score 20; DB 2; Length 2034;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 81 GCTCTGGGGGATCTGTCC 100
DB 803 GCTCTGGGGGATCTGTCC 822
```

```
RESULT 12
US-09-621-976-8768/c
; Sequence 8768, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8768
; LENGTH: 448
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8768
```

```
Query Match 2.1%; Score 19; DB 4; Length 448;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 505 CATCTCAGGACCCACGC 523
DB 387 CATCTCAGGACCCACGC 369
```

```
RESULT 13
US-09-621-976-8742/c
; Sequence 8742, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8742
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 225
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-8742
```

```
Query Match 2.1%; Score 19; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 505 CATCTCAGGACCCACGC 523
DB 389 CATCTCAGGACCCACGC 371
```

```
RESULT 14
US-09-621-976-8732/c
; Sequence 8732, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8732
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8732
```

```
Query Match 2.1%; Score 19; DB 4; Length 465;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 505 CATCTCAGGACCCACGC 523
DB 397 CATCTCAGGACCCACGC 379
```

```
RESULT 15
US-09-621-976-8667/c
; Sequence 8667, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
```

```

; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8667
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8667

```

```

Query Match      2.1%; Score 19; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      505 CATTCGAGGACCCACGC 523
Db      394 CATTCGAGGACCCACGC 376

```

Search completed: January 11, 2005, 11:40:27
Job time : 114 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 11, 2005, 09:25:21 ; Search time 596 Seconds
(without alignments)
8577.830 Million cell updates/sec

Title: US-09-994-365-1
Perfect score: 891
Sequence: 1 ccccttgggggttcccgagca.....taaaatcatgttctcttaa 891

Scoring table: OLIGO_NIC
Gapop 60.0 , Gapext 60.0

Searched: 4293498 seqs, 2868903791 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8586996

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Published Applications NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	891	100.0	891	9 US-09-994-365-1	Sequence 1, Appl1
2	775	87.0	2997	9 US-09-994-365-10	Sequence 10, Appl1
3	775	87.0	3001	9 US-09-994-365-4	Sequence 4, Appl1
4	724	81.3	25235	15 US-10-164-230-2	Sequence 2, Appl1
5	724	81.3	55050	17 US-10-467-752-4	Sequence 4, Appl1
6	554	62.2	157	15 US-10-029-386-5700	Sequence 5700, Ap
7	157	17.6	157	15 US-10-029-386-19510	Sequence 19510, A
8	60	6.7	60	10 US-09-908-975-5077	Sequence 5077, Ap
9	50	5.6	50	16 US-10-131-827-532	Sequence 532, App
c 10	33	3.7	3673778	15 US-10-312-841-1	Sequence 11, Appl1
11	21	2.4	21	9 US-09-994-365-11	Sequence 11, Appl1
12	21	2.4	3673778	15 US-10-312-841-2	Sequence 2, Appl1

C 13	20	2.2	331	9 US-09-960-352-3940	Sequence 3940, Ap
C 14	20	2.2	335	9 US-09-960-352-5881	Sequence 5881, Ap
C 15	20	2.2	411	9 US-09-960-352-4663	Sequence 4663, Ap
C 16	20	2.2	531	10 US-09-918-995-25552	Sequence 25552, A
C 17	20	2.2	636	13 US-10-027-632-140159	Sequence 140159, A
C 18	20	2.2	636	13 US-10-027-632-140160	Sequence 140160, A
C 19	20	2.2	636	15 US-10-027-632-140159	Sequence 140159, A
C 20	20	2.2	636	15 US-10-027-632-140160	Sequence 140160, A
C 21	20	2.2	636	15 US-10-027-632-140160	Sequence 140160, A
C 22	20	2.2	925	17 US-10-437-963-25592	Sequence 25592, A
C 23	20	2.2	1740	16 US-10-641-643-1110	Sequence 1110, Ap
C 24	20	2.2	2167	15 US-10-094-749-145	Sequence 145, App
C 25	20	2.2	202814	18 US-10-719-993-6812	Sequence 6812, Ap
C 26	20	2.2	1601042	13 US-10-027-632-59064	Sequence 59064, A
C 27	20	2.2	1601042	15 US-10-027-632-59064	Sequence 59064, A
C 28	19	2.1	19	9 US-09-994-365-12	Sequence 12, Appl1
C 29	19	2.1	385	10 US-09-803-719-2243	Sequence 2243, Ap
C 30	19	2.1	458	9 US-09-864-761-10055	Sequence 10055, A
C 31	19	2.1	876	16 US-10-424-599-74654	Sequence 74654, A
C 32	19	2.1	1059	13 US-10-027-632-119721	Sequence 119721, A
C 33	19	2.1	1059	13 US-10-027-632-119722	Sequence 119722, A
C 34	19	2.1	1059	13 US-10-027-632-119723	Sequence 119723, A
C 35	19	2.1	1059	15 US-10-027-632-119721	Sequence 119721, A
C 36	19	2.1	1059	15 US-10-027-632-119722	Sequence 119722, A
C 37	19	2.1	1059	15 US-10-027-632-119723	Sequence 119723, A
C 38	19	2.1	15853	16 US-10-221-613-422	Sequence 422, App
C 39	19	2.1	59588	15 US-10-017-161-2223	Sequence 2223, Ap
C 40	19	2.1	59588	15 US-10-292-798-1879	Sequence 1879, Ap
C 41	19	2.1	73145	13 US-10-087-192-274	Sequence 274, App
C 42	19	2.1	87394	18 US-10-810-788A-6	Sequence 6, Appl1
C 43	19	2.1	110079	14 US-10-175-523-96	Sequence 96, Appl1
C 44	19	2.1	197526	17 US-10-322-281-498	Sequence 498, App
C 45	18	2.0	18	15 US-10-164-230-23	Sequence 23, Appl1

ALIGNMENTS

RESULT 1
US-09-994-365-1
; Sequence 1, Application US/0994365
; Patent No. US20020115148A1
; GENERAL INFORMATION:
; APPLICANT: Charmsley, Patrick
; APPLICANT: Mose, Patrick
; APPLICANT: McBurn, Mark
; TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
; FILE REFERENCE: CECH118109
; CURRENT APPLICATION NUMBER: US/09/994,365
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 60/253,592
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/256,839
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(471)
US-09-994-365-1

Query Match 100.0%; Score 891; DB 9; Length 891;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTTGGGGGTTCCCGAGCAGCCAGCTCAGCCAGCTTTGGGGCCGATCATTA 60
DB 1 CCTCTTGGGGGTTCCCGAGCAGCCAGCTCAGCCAGCTTTGGGGCCGATCATTA 60

QY 61 GCCATGATCTCTCAACCTGAGAGCTCTGGAGTCTTGCTCTTGCTCTGACACAGAGAGC 120
 DB 61 GCCATGATCTCTCAACCTGAGAGCTCTGGAGTCTTGCTCTTGCTCTGACACAGAGAGC 120
 QY 121 ATCTCAGGACGAGAGGAGCAGCCTCTCTCAACCTGAGAGAGAGAGAGAGAGAGC 180
 DB 121 ATCTCAGGACGAGAGGAGCAGCCTCTCTCAACCTGAGAGAGAGAGAGAGAGAGC 180
 QY 181 TCCCAACATTTGCTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
 DB 181 TCCCAACATTTGCTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
 QY 241 CTCTTTGAGAGATCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAG 300
 DB 241 CTCTTTGAGAGATCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAG 300
 QY 301 GGAATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
 DB 301 GGAATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
 QY 361 CCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
 DB 361 CCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
 QY 421 AACGACCTCAG 480
 DB 421 AACGACCTCAG 480
 QY 481 CCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
 DB 481 CCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
 QY 541 TCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
 DB 541 TCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
 QY 601 TTTATTTCTGAACCGGTAAAGTGTGTCTCAATTTCTGCTGCTCTGAGATCCATA 660
 DB 601 TTTATTTCTGAACCGGTAAAGTGTGTCTCAATTTCTGCTGCTCTGAGATCCATA 660
 QY 661 CTGAGTCTCTCAACCGGCTTTTCTCTGAGAGGCTAAAGCTCTCTCTCTCTCTCTCTCT 720
 DB 661 CTGAGTCTCTCAACCGGCTTTTCTCTGAGAGGCTAAAGCTCTCTCTCTCTCTCTCTCT 720
 QY 721 CTCGAGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
 DB 721 CTCGAGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
 QY 781 CAGGAGCTATGTATGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
 DB 781 CAGGAGCTATGTATGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
 QY 841 AGACAGCTGCT 891
 DB 841 AGACAGCTGCT 891

RESULT 2
 US-09-994-365-10
 ; Sequence 10, Application US/09994365
 ; Patent No. US20020115148A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Charmley, Patrick
 ; APPLICANT: Moss, Patrick
 ; APPLICANT: McSuen, Mark
 ; TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Peptidiasis
 ; FILE REFERENCE: CECH18109
 ; CURRENT APPLICATION NUMBER: US/09/994,365
 ; PRIOR FILING DATE: 2001-11-26
 ; PRIOR APPLICATION NUMBER: US 60/253,592
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: US 60/256,839
 ; PRIOR FILING DATE: 2000-12-15

; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 2997
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-994-365-10
 Query Match 87.0%; Score 775; DB 9; Length 2997;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 775; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 117 AGCATCTCAG 176
 DB 1200 AGCATCTCAG 2259
 QY 177 AGGCTCCCAACATTTGCTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 236
 DB 2260 AGGCTCCCAACATTTGCTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2319
 QY 237 CCTCTCTTTGAGAGATCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAG 296
 DB 2320 CCTCTCTTTGAGAGATCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAGAGCTCTGAG 2379
 QY 297 AACTGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 356
 DB 2380 AACTGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2439
 QY 357 CGACCTTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 416
 DB 2440 CGACCTTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2499
 QY 417 GGAACAACGAGCTCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 476
 DB 2500 GGAACAACGAGCTCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2559
 QY 477 GAGTCCCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 536
 DB 2560 GAGTCCCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2619
 QY 537 TGATTTCCGAGTAAATTTCTCTCAATTTCTCTCAATTTCTCTCAATTTCTCTCAATTT 596
 DB 2620 TGATTTCCGAGTAAATTTCTCTCAATTTCTCTCAATTTCTCTCAATTTCTCTCAATTT 2679
 QY 597 CGATTTATTTCTGAACCGGTAAAGTGTGTCTCAATTTCTCTCAATTTCTCTCAATTTCT 656
 DB 2680 CGATTTATTTCTGAACCGGTAAAGTGTGTCTCAATTTCTCTCAATTTCTCTCAATTTCT 2739
 QY 657 CATACTTACTCTCATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 716
 DB 2740 CATACTTACTCTCATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2799
 QY 717 TGGCTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 776
 DB 2800 TGGCTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2859
 QY 777 GGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 836
 DB 2860 GGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2919
 QY 837 CAGTAGACAGCTGCT 891
 DB 2920 CAGTAGACAGCTGCT 2974

RESULT 3
 US-09-994-365-4
 ; Sequence 4, Application US/09994365
 ; Patent No. US20020115148A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Charmley, Patrick
 ; APPLICANT: Moss, Patrick
 ; APPLICANT: McSuen, Mark

QY 357 CGACCTTGGCCGAGAGACCCACCCGAGAAAAACCCCTGACCTCTGCTCCCTGAGGT 416
DB 1993 CGACCTTGGCCGAGAGACCCACCCGAGAAAAACCCCTGACCTCTGCTCCCTGAGGT 2052
QY 417 GGAACACCGACTCAGAGAGAGCCAGACCTTGAACCCCGGAGAAAGTACATATATG 476
DB 2053 GGAACACCGACTCAGAGAGAGCCAGACCTTGAACCCCGGAGAAAGTACATATATG 2112
QY 477 GAGTCCCTCAGACCGCTTCTGTTCCAGAGACCTTCAAGGACCCAGGCGCTCTCCAGCCTC 536
DB 2113 GAGTCCCTCAGACCGCTTCTGTTCCAGAGACCTTCAAGGACCCAGGCGCTCTCCAGCCTC 2172
QY 537 TGATTCCTCGTAATCTTCTCCCAATTTAGCCTATCTCTTAACCTTCTCTCAATTCCT 596
DB 2173 TGATTCCTCGTAATCTTCTCCCAATTTAGCCTATCTCTTAACCTTCTCTCAATTCCT 2232
QY 597 CGGTTTATCTGAACCCGTAAGGTGATGTTCTCAATTTCTCTGCTCCCTCTGAGATC 656
DB 2233 CGGTTTATCTGAACCCGTAAGGTGATGTTCTCAATTTCTCTGCTCCCTCTGAGATC 2292
QY 657 CATACTTAGTCTCAGATCCGCGCTTTTCTCTGACAGCTTAAGCTTACTCTTACC 716
DB 2293 CATACTTAGTCTCAGATCCGCGCTTTTCTCTGACAGCTTAAGCTTACTCTTACC 2352
QY 717 TCGCTCTCAGGCTCTGCGCCCACTTACCTCCACCCGCTCTTCTGCGCGGAGTGGT 776
DB 2353 TCGCTCTCAGGCTCTGCGCCCACTTACCTCCACCCGCTCTTCTGCGCGGAGTGGT 2412
QY 777 GGGGACAGGCTATGATGATGTTGCTCTGACAGCTGATGAGCGGCGGACAGAACTAT 836
DB 2413 GGGGACAGGCTATGATGATGTTGCTCTGACAGCTGATGAGCGGCGGACAGAACTAT 2472
QY 837 CAGTAGACAGCTGCTGCTTCATGAAACGAAATAATCAATGTTTCTTAA 891
DB 2473 CAGTAGACAGCTGCTGCTTCATGAAACGAAATAATCAATGTTTCTTAA 2527

RESULT 5

US-10-467-752-4
; Sequence 4, Application US/10467752
; Publication No. US20040161759A1
; GENERAL INFORMATION:
; APPLICANT: Lench, et al.
; TITLE OF INVENTION: Test and Model for Inflammatory disease
; FILE REFERENCE: 2003882-0009
; CURRENT APPLICATION NUMBER: US/10/467, 752
; CURRENT FILING DATE: 2003-08-13
; PRIOR APPLICATION NUMBER: PCT/GB02/00653
; PRIOR FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: GB0103514.6
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 55050
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13351)..(13351)
; OTHER INFORMATION: n is a or t or g or c
; NAME/KEY: misc feature
; LOCATION: (13401)..(13401)
; OTHER INFORMATION: n is a or t or g or c
US-10-467-752-4

Query Match 81.3%; Score 724; DB 17; Length 55050;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 774; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 117 AGGCATCTCAGGAGGAGGAGCCGCTCTCAGCCACCGGAGAGAGAGAGG 176
|||||

DB 27098 AGGCATCTCAGGAGGAGGAGCCACCCCTTCAACCCAGCCGAGAGAGAGAGG 27157
QY 177 AGGTCCTCCCACTTGGCTTCAAGGCCCCCGAGTCCCGGTGACCTTTGGCAGAGGAC 236
DB 27158 AGGTCCTCCCACTTGGCTTCAAGGCCCCCGAGTCCCGGTGACCTTTGGCAGAGGAC 27217
QY 237 CCCTCTCTTGAAGATCTCTCGCTTACCCGCCCCAGTCCCTCTGAGAGACTGCTGA 296
DB 27218 CCCTCTCTTGAAGATCTCTCGCTTACCCGCCCCAGTCCCTCTGAGAGACTGCTGA 27277
QY 297 AACTGAGTGTGCCCCCTTGAACCGCTTGAACGATTCCTCTGAACCTTCCCGCTGA 356
DB 27278 AACTGAGTGTGCCCCCTTGAACCGCTTGAACGATTCCTCTGAACCTTCCCGCTGA 27337
QY 357 CGACCTTGGCCGAGAGACCCAGGCCCCGAGAAACCCCTGAGCTCTGCGCCCTGAGGT 416
DB 27338 CGACCTTGGCCGAGAGACCCAGGCCCCGAGAAACCCCTGAGCTCTGCGCCCTGAGGT 27397
QY 417 GGAACACCGACTCAGAGAGAGCCAGACCTTGAACCCAGGAGAGATACATATATG 476
DB 27398 GGAACACCGACTCAGAGAGAGCCAGACCTTGAACCCAGGAGAGATACATATATG 27457
QY 477 GAGTCCCTCAGACCGCTTCTGTTCCAGAGATCTTCAAGGACCCAGGCGCTCTCAACCTC 536
DB 27458 GAGTCCCTCAGACCGCTTCTGTTCCAGAGATCTTCAAGGACCCAGGCGCTCTCAACCTC 27517
QY 537 TGATTCCTCGTAATCTTCTCCCAATTTAGCCTATCTCTTAACCTTCTCTCAATTCCT 596
DB 27518 TGATTCCTCGTAATCTTCTCCCAATTTAGCCTATCTCTTAACCTTCTCTCAATTCCT 27577
QY 597 CGGTTTATCTGAACCCGTAAGGTGATGTTCTCAATTTCTCTGCTCCCTCTGAGATC 656
DB 27578 CGGTTTATCTGAACCCGTAAGGTGATGTTCTCAATTTCTCTGCTCCCTCTGAGATC 27637
QY 657 CATACTTAGTCTCAGATCCGCGCTTTTCTCTGACAGCTTAAGCTTACTCTTACC 716
DB 27638 CATACTTAGTCTCAGATCCGCGCTTTTCTCTGACAGCTTAAGCTTACTCTTACC 27697
QY 717 TCGCTCTCAGGCTCTGCGCCCACTTACCTCCACCCGCTCTTCTGCGCGGAGTGGT 776
DB 27698 TCGCTCTCAGGCTCTGCGCCCACTTACCTCCACCCGCTCTTCTGCGCGGAGTGGT 27757
QY 777 GGGGACAGGCTATGATGATGTTGCTCTGACAGCTGATGAGCGGCGGACAGAACTAT 836
DB 27758 GGGGACAGGCTATGATGATGTTGCTCTGACAGCTGATGAGCGGCGGACAGAACTAT 27817
QY 837 CAGTAGACAGCTGCTGCTTCATGAAACGAAATAATCAATGTTTCTTAA 891
DB 27818 CAGTAGACAGCTGCTGCTTCATGAAACGAAATAATCAATGTTTCTTAA 27872

RESULT 6

US-10-029-386-5700
; Sequence 5700, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029, 386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 5700
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB023060.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.82
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.82
 OTHER INFORMATION: SWISSPROT HIT: B9513178.1, EVALUATE 0.00e+00
 OTHER INFORMATION: EST_HUMAN HIT: B9513178.1, EVALUATE 0.00e+00
 OTHER INFORMATION: NT HIT: g115304354, EVALUATE 0.00e+00
 US-10-029-386-5700

Query Match 62.2%; Score 554; DB 15; Length 565;
 Best Local Similarity 100.0%; Pred. No. 5.8e-279; Indels 0; Gaps 0;
 Matches 554; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 CCCCCTCTTTGAAAGTCTCCGCTAACCCGCCAGATGCTCCCTGAGAGACCTGCT 294
 Db 1 CCCCCTCTTTGAAAGTCTCCGCTAACCCGCCAGATGCTCCCTGAGAGACCTGCT 60
 QY 295 GAAACTGAGTCTGCCCCCTTGAACCCGCTTGAACCGATCTCTCACTCCCGGCT 354
 Db 61 GAAACTGAGTCTGCCCCCTTGAACCCGCTTGAACCGATCTCTCACTCCCGGCT 120
 QY 355 GACGACCTTGGCCGCGAGAGACCCAGCCCGCAGAAAACCCCTGCTCCCTGAG 414
 Db 121 GACGACCTTGGCCGCGAGAGACCCAGCCCGCAGAAAACCCCTGCTCCCTGAG 180
 QY 415 GTGAGAACCGACCTCAGAGAGACCACTAGACCCAGCCGGAAGAGTACAGATAA 474
 Db 181 GTGAGAACCGACCTCAGAGAGACCACTAGACCCAGCCGGAAGAGTACAGATAA 240
 QY 475 TGAAGTCCCTCAGACCTTCTGTTCCAGAGCATCTCCAGAGACCCGCTTCCACC 534
 Db 241 TGAAGTCCCTCAGACCTTCTGTTCCAGAGCATCTCCAGAGACCCGCTTCCACC 300
 QY 535 TCTGATCCCCCGTGAATTTCTCCCAATTTAGCCTATCTCTTAACCTCTTCCATTC 594
 Db 301 TCTGATCCCCCGTGAATTTCTCCCAATTTAGCCTATCTCTTAACCTCTTCCATTC 360
 QY 595 CTGGGTTTATTTGAAACCCGTAAGTGTGTTCTCAATATTTCTGCTCCCTCAGAG 654
 Db 361 CTGGGTTTATTTGAAACCCGTAAGTGTGTTCTCAATATTTCTGCTCCCTCAGAG 420
 QY 655 TCCATATTTAGTCTCAGATGCCCCGTTTTTCTCTGAGACGCTTACCTCTCTTA 714
 Db 421 TCCATATTTAGTCTCAGATGCCCCGTTTTTCTCTGAGACGCTTACCTCTCTTA 480
 QY 715 CCTGCTCCAGAGCTGCGGCCCACTACCTCCAGCCGAGTCTCTGCCCCGCGATCG 774
 Db 481 CCTGCTCCAGAGCTGCGGCCCACTACCTCCAGCCGAGTCTCTGCCCCGCGATCG 540
 QY 775 CTGGGCGAGGCTTA 788
 Db 541 CTGGGCGAGGCTTA 554

RESULT 7
 US-10-029-386-19510
 Sequence 19510, Application US/10029386
 Publication No. US20030194704A1

GENERAL INFORMATION:
 APPLICANT: Penn, Sharon G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
 FILE REFERENCE: A60MICA-X-2
 CURRENT APPLICATION NUMBER: US/10/029,386
 CURRENT FILING DATE: 2001-12-20
 NUMBER OF SEQ ID NOS: 34288
 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 SEQ ID NO 19510
 LENGTH: 157
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AB023060.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.82
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.82
 OTHER INFORMATION: SWISSPROT HIT: P13889, EVALUATE 3.00e-01
 US-10-029-386-19510

Query Match 17.6%; Score 157; DB 15; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.5e-71; Indels 0; Gaps 0;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 318 ACCGCTAGAACGATCTCTCAACCTCCCGGCTGAGACCTTGGCGGAGGACC 377
 Db 1 ACCGCTAGAACGATCTCTCAACCTCCCGGCTGAGACCTTGGCGGAGGACC 60
 QY 378 CAGACCCCGAAGAAACCCCTGCTCTCTGCTCCCTGAGTGAACAACGACTCAGAGGA 437
 Db 61 CAGACCCCGAAGAAACCCCTGCTCTCTGCTCCCTGAGTGAACAACGACTCAGAGGA 120
 QY 438 GCCAGACTAGACCCAGCCGCGGAGAGTACAGATAA 474
 Db 121 GCCAGACTAGACCCAGCCGCGGAGAGTACAGATAA 157

RESULT 8
 US-09-908-975-5077
 Sequence 5077, Application US/09908975
 Publication No. US20030165843A1

GENERAL INFORMATION:
 APPLICANT: SHOSHAN, Avi
 APPLICANT: WASSEMAN, Alon
 APPLICANT: MINTZ, Eli
 APPLICANT: FAIGLER, Simchon
 TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
 FILE REFERENCE: 36688-0005
 CURRENT APPLICATION NUMBER: US/09/908,975
 CURRENT FILING DATE: 2001-07-20
 PRIOR APPLICATION NUMBER: US 60/287,724
 PRIOR FILING DATE: 2001-05-02
 PRIOR APPLICATION NUMBER: US 60/221,607
 PRIOR FILING DATE: 2000-07-28
 NUMBER OF SEQ ID NOS: 32337
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 5077
 LENGTH: 60
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-908-975-5077

Query Match 6.7%; Score 60; DB 10; Length 60;
 Best Local Similarity 100.0%; Pred. No. 1.4e-20; Indels 0; Gaps 0;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 GCCCTCCACCCCTGATTCCTCCGGAATTTCTCCCAATTTAGCCATCTCCTTAAC 581
 Db 1 GCCCTCCACCCCTGATTCCTCCGGAATTTCTCCCAATTTAGCCATCTCCTTAAC 60

RESULT 9
 US-10-131-827-532
 Sequence 532, Application US/10131827
 Publication No. US20040009479A1

GENERAL INFORMATION:
 APPLICANT: Wohlgenuth, Jay
 APPLICANT: Fry, Kirk
 APPLICANT: Woodward, Robert
 APPLICANT: Ly, Ngoc
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
 FILE REFERENCE: 506612000120

```
/ CURRENT APPLICATION NUMBER: US/10/131,827
/ CURRENT FILING DATE: 2002-09-06
/ PRIOR APPLICATION NUMBER: US 10/006,290
/ PRIOR FILING DATE: 2001-10-22
/ PRIOR APPLICATION NUMBER: US 60/296,764
/ PRIOR FILING DATE: 2001-06-08
/ NUMBER OF SEQ ID NOS: 9090
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 532
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-131-827-532
```

```
Query Match
Best Local Similarity 100.0%; Score 50; DB 16; Length 50;
Pred. No. 2.5e-15;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 820 CCGCGCGGAGAGACTATGATGAGACAGCTGCTTCATGAAACGAAA 869
DB 1 CCGCGCGGAGAGACTATGATGAGACAGCTGCTTCATGAAACGAAA 50
```

```
RESULT 10
US-10-312-841-1/C
/ Sequence 1, Application US/10312841
/ Publication No. US20030186277A1
/ GENERAL INFORMATION:
/ APPLICANT: Epigenomics AG
/ TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
/ FILE REFERENCE: E01/1208/WO
/ CURRENT APPLICATION NUMBER: US/10/312,841
/ NUMBER OF SEQ ID NOS: 2
/ SEQ ID NO 1
/ LENGTH: 3673778
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens).
/ NAME/KEY: unsure
/ LOCATION: (3294164)
US-10-312-841-1
```

```
Query Match
Best Local Similarity 100.0%; Score 33; DB 15; Length 3673778;
Pred. No. 6.4e-07;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 566 CCTATCTCCTTAAACCTCTTCCTCATTCCTCG 598
DB 1425602 CCTATCTCCTTAAACCTCTTCCTCATTCCTCG 1425570
```

```
RESULT 11
US-09-994-365-11
/ Sequence 11, Application US/09994365
/ Patent No. US20020115148A1
/ GENERAL INFORMATION:
/ APPLICANT: Charmley, Patrick
/ APPLICANT: Moss, Patrick
/ APPLICANT: McEuen, Mark
/ TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
/ FILE REFERENCE: CECH18109
/ CURRENT APPLICATION NUMBER: US/09/994,365
/ CURRENT FILING DATE: 2001-11-26
/ PRIOR APPLICATION NUMBER: US 60/253,592
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US 60/256,839
/ PRIOR FILING DATE: 2000-12-15
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 11
```

```
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(21)
/ OTHER INFORMATION: PCR Primer DMO 9299
US-09-994-365-11
```

```
Query Match
Best Local Similarity 100.0%; Score 21; DB 9; Length 21;
Pred. No. 3.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 25 GACTCAGCCGCCAGCTTT 45
DB 1 GACTCAGCCGCCAGCTTT 21
```

```
RESULT 12
US-10-312-841-2
/ Sequence 2, Application US/10312841
/ Publication No. US20030186277A1
/ GENERAL INFORMATION:
/ APPLICANT: Epigenomics AG
/ TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
/ FILE REFERENCE: E01/1208/WO
/ CURRENT APPLICATION NUMBER: US/10/312,841
/ CURRENT FILING DATE: 2002-12-30
/ NUMBER OF SEQ ID NOS: 2
/ SEQ ID NO 2
/ LENGTH: 3673778
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
/ NAME/KEY: unsure
/ LOCATION: (379615)
US-10-312-841-2
```

```
Query Match
Best Local Similarity 100.0%; Score 21; DB 15; Length 3673778;
Pred. No. 1.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 858 ATGAAACGAAAAATATAAT 878
DB 2248469 ATGAAACGAAAAATATAAT 2248489
```

```
RESULT 13
US-09-960-352-3940/C
/ Sequence 3940, Application US/09960352
/ Patent No. US20020137139A1
/ GENERAL INFORMATION:
/ APPLICANT: Warren, Wesley C.
/ APPLICANT: Tao, Nengbing
/ APPLICANT: Byatt, John C.
/ APPLICANT: Mathiasagan, Nagappan
/ TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
/ FILE REFERENCE: 16511.006/37-21(10298)C
/ CURRENT APPLICATION NUMBER: US/09/960,352
/ CURRENT FILING DATE: 2001-09-24
/ NUMBER OF SEQ ID NOS: 15112
/ SEQ ID NO 3940
/ LENGTH: 331
/ TYPE: DNA
/ ORGANISM: Bos taurus
/ OTHER INFORMATION: Clone ID: 17-LIB34-027-Q1-E1-E9
US-09-960-352-3940
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 331;
Pred. No. 10;
```

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCAGGGCCCCCAGTCCCG 214
 |||||
 Db 63 TCAGGGCCCCCAGTCCCG 44

RESULT 14

US-09-960-352-5881/C
 ; Sequence 5881, Application US/09960352
 ; Patent No. US20020137139A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Warren, Wesley C.
 ; APPLICANT: Tao, Nengbing
 ; APPLICANT: Byatt, John C.
 ; APPLICANT: Mathialagan, Nagappan
 ; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
 ; FILE REFERENCE: 16511.006/37-21(10298)C
 ; CURRENT APPLICATION NUMBER: US/09/960,352
 ; CURRENT FILING DATE: 2001-09-24
 ; NUMBER OF SEQ ID NOS: 15112
 ; SEQ ID NO 5881
 ; LENGTH: 395
 ; TYPE: DNA
 ; ORGANISM: Bos taurus
 ; OTHER INFORMATION: Clone ID: 25-LIB34-044-Q1-E1-G1
 US-09-960-352-5881

Query Match 2.2%; Score 20; DB 9; Length 395;
 Best Local Similarity 100.0%; Pred. No. 9.8;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCAGGGCCCCCAGTCCCG 214
 |||||
 Db 72 TCAGGGCCCCCAGTCCCG 53

RESULT 15

US-09-960-352-4663/C
 ; Sequence 4663, Application US/09960352
 ; Patent No. US20020137139A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Warren, Wesley C.
 ; APPLICANT: Tao, Nengbing
 ; APPLICANT: Byatt, John C.
 ; APPLICANT: Mathialagan, Nagappan
 ; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
 ; FILE REFERENCE: 16511.006/37-21(10298)C
 ; CURRENT APPLICATION NUMBER: US/09/960,352
 ; CURRENT FILING DATE: 2001-09-24
 ; NUMBER OF SEQ ID NOS: 15112
 ; SEQ ID NO 4663
 ; LENGTH: 411
 ; TYPE: DNA
 ; ORGANISM: Bos taurus
 ; OTHER INFORMATION: Clone ID: 20-LIB34-020-Q1-E2-E7
 US-09-960-352-4663

Query Match 2.2%; Score 20; DB 9; Length 411;
 Best Local Similarity 100.0%; Pred. No. 9.8;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCAGGGCCCCCAGTCCCG 214
 |||||
 Db 349 TCAGGGCCCCCAGTCCCG 330

Search completed: January 11, 2005, 11:50:40
 Job time : 609 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 11, 2005, 09:34:16 ; Search time 431.936 Seconds
(without alignments)
1652.840 Million cell updates/sec

Title: US-09-994-365-2
Perfect score: 808
Sequence: 1 MIMMKLIGLIVCLHTRGI.....EVDNRPOEPDLPDPREYR 136

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 413486 segs, 2624710521 residues
Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRY=xlh
-Q=/cgn2_1/USPTO.spool_h/US0994365/runat_10012005_172231_6815/app.query.fasta_1.590
-DB=N.GeneSeq_23Sep04 -OFMT=faclap -SUFFIX=p2n.rng -MIMMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=plc -NOB=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US0994365.qcch_1.1.586 @runat_10012005_172231_6815 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESUBTRY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOCK
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: N.GeneSeq_23Sep04:*
2: geneeqn1980s:*
3: geneeqn1990s:*
4: geneeqn2000s:*
5: geneeqn2001as:*
6: geneeqn2001bs:*
7: geneeqn2002as:*
8: geneeqn2002bs:*
9: geneeqn2003as:*
10: geneeqn2003bs:*
11: geneeqn2003ds:*
12: geneeqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	808	100.0	891	6	ABK86962 Human can
2	808	100.0	1473	6	ABN60006 Novel hum
3	712	88.1	2997	6	ABK86967 Human CAN
4	712	88.1	3001	6	ABK86963 Human CAN
5	712	88.1	25235	4	AAH45310 Human SEE
6	712	88.1	55050	6	ABQ75680 Human SEE

7	486	60.1	565	12	ACH72505	Ach72505 Human gen
8	314	38.9	157	12	ACH86315	Ach86315 Human gen
9	199	24.6	711	8	ACA43990	Aca43990 Prokaryot
10	198.5	24.6	2772	8	ACA40420	Aca40420 Prokaryot
11	198.5	24.6	110000	4	AAI99682_10	Continuation (11 o
12	198.5	24.6	110000	4	AAI99683_10	Continuation (11 o
13	195.5	24.2	446	4	AAI23276	Probe #13
14	195.5	24.2	446	4	ABA68382	Human foe
15	195.5	24.2	446	4	AAI48596	Probe #17
16	195.5	24.2	446	4	ABA50433	Human bre
17	195.5	24.2	446	4	ABA53379	Probe #13
18	195.5	24.2	446	4	AAK42529	Human bon
19	195.5	24.2	446	4	AAK16757	Human bra
20	195.5	24.2	446	4	ABS42140	Human liv
21	195.5	24.2	446	5	AAI08921	Probe #89
22	195.5	24.2	446	6	ABS16574	Human gen
23	195	24.1	12733	6	ABK98631	Vector pr
24	195	24.1	12733	6	ACD13882	L. lactis
25	195	24.1	12739	6	ABK98592	Vector pr
26	195	24.1	12739	2	ACD13843	Plasmid p
27	190.5	23.6	6313	2	AAO29965	Sugar bee
28	189.5	23.5	110000	4	AAI99682_09	Continuation (10 o
29	189.5	23.5	110000	4	AAI99683_09	Continuation (10 o
30	188.5	23.3	600	6	ABQ52497	Abq52497 Oligonuc
31	188.5	23.3	600	6	ABQ52496	Abq52496 Oligonuc
32	188.5	23.3	110000	4	AAI99682_27	Continuation (28 o
33	188.5	23.3	110000	4	AAI99683_28	Continuation (28 o
34	188.5	23.3	110000	4	AAI99683_27	Continuation (28 o
35	188	23.3	1493	12	ACH91938	Human gen
36	187.5	23.2	1327	6	ABQ68452	Abq68452 Listeria
37	187.5	23.2	3946	2	AAI93610	Myobacte
38	187	23.1	1833	4	ABL22159	Drosophi
39	186	23.0	1452	8	ACF39367	Myobacte
40	186	23.0	1455	8	ACA40813	Prokaryot
41	186	23.0	110000	4	AAI99682_37	Continuation (38 o
42	186	23.0	110000	4	AAI99683_37	Continuation (38 o
43	185	22.9	110000	4	AAI99682_40	Continuation (41 o
44	185	22.9	110000	4	AAI99683_40	Continuation (41 o
45	184.5	22.8	110000	4	AAI99683_11	Continuation (12 o

ALIGNMENTS

RESULT 1	
ID	ABK86962 standard; CDNA; 891 BP.
XX	ABK86962;
AC	
XX	
DT	24-SEP-2002 (first entry)
XX	
DE	Human candidate coding sequence-1 (CAN-1) CDNA.
XX	
KW	Human; antiapoptotic; chromosome 6; candidate coding sequence-1; CAN-1;
KW	SEER-1; STG; human leukocyte antigen C; HLA C; HLA Cw6; psoriasis; skin;
KW	keratinocyte; chronic inflammatory dermatosis; erythroderma; seborethic;
KW	gutrate; pustular variant; Reiter's disease; hyperproliferation;
KW	epidermis; differentiation; diagnosis; gene therapy; gene; ss; SNF;
KW	single nucleotide polymorphism.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	64..474
FT	/*tag= a
FT	/product= "CAN-1"
FT	64..129
FT	sig_peptide
FT	/*tag= b
FT	130..471
FT	mat_peptide
FT	/*tag= c
FT	/note= "Mature CAN-1"
FT	variation
FT	/*tag= d

FT	/standard_name= "Single nucleotide polymorphism"
XX	
XX	
PN	MO200244375-A2.
XX	
XX	
PD	06-JUN-2002.
XX	
XX	
PF	27-NOV-2001; 2001MO-US044506.
XX	
XX	
PR	28-NOV-2000; 2000US-0253592P.
PR	15-DEC-2000; 2000US-0256839P.
XX	
XX	
PA	(CELL-) CELUTECH R & D INC.
XX	
PI	Charmley P, `Moss P, Mceuen M;
XX	
XX	
DR	WPI; 2002-508513/54.
DR	P-PSDB; AAU79579.
XX	
XX	
PT	Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation
PT	and differentiation, and polynucleotides encoding the polypeptide; useful
PT	for diagnosing or predicting susceptibility to psoriasis in individual.
XX	
XX	
PS	Claim 8; Page 80-81; 95pp. English.

The invention discloses isolated candidate coding sequence-1 (CAN-1), SEER-1 (not defined) and STG (not defined) polypeptides, and the polynucleotides encoding them. All three genes were identified due to their proximity to the human leukocyte antigen C (HLA C) locus on chromosome 6. The HLA Cw6 allele is associated with psoriasis and as the three genes are expressed in normal skin and/or keratinocyte tissue, they may also have a role in psoriasis. Psoriasis is a chronic inflammatory dermatosis that is characterized by hyperproliferation of epidermal cells. Possible treatments against psoriasis involve the inhibition of movement of cells into the epidermis, or the inhibition of hyperproliferation or abnormal differentiation of keratinocytes, by the inhibition of the CAN-1, STG or SEER-1 polypeptides binding to their binding partners. The polypeptides are useful for diagnosing or predicting the susceptibility to psoriasis in an individual, for ameliorating the symptoms and/or progression of psoriasis and for identifying agents useful for treating psoriasis or modulating the activity of the polypeptide. The polypeptides are also useful for enhancing the level of CAN-1, STG or SEER-1 biological activity in a cell or tissue. The nucleic acid molecules are useful as hybridisation probes in diagnostic procedures (such as diagnosing the presence of psoriasis or the propensity to develop psoriasis) and for suppressing the expression of CAN-1 or STG gene (e.g. antisense inhibition, gene therapy). Antibodies, raised against the polypeptides, are useful for decreasing the level of CAN-1, STG or SEER-1 biological activity in a cell. The sequence presented is the human candidate coding sequence-1 (CAN-1) cDNA

Alignment Scores:	
Pred. No.:	6.84e-29
Score:	808.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	6
	Gaps:
	0

US-09-994-365-2 (1-136) x ABRK6962 (1-891)

Qy	Db	Qy	Db	Qy	Db
20	122	40	185	60	243
MeTtIeLeuAeNtTrrpYsLeuEugLylIeLeuValLeuSueLhNtStHAtgUlyLe	ATATCTCTCACTGGAAAGCTCTGGGAGATCTGGCTCTTGTCTCAACACAGAGGACTC	SerGISeRcIuGtYhIsProSeRtHsPProFolAGtAAsPAtgUgUaLgLySer	TCAGGACAGCGAGGCCACCCCTCTCAACCCCGAGAGAGACCGAGAGAGCGAGGCTCC	ProThrLeuProGInGlyProProValAlProGlyAspProTrrProGlyAlAProProLeu	CCAACTTGTGCTCAGGCGCCCCCAAGTCCCCGATGACCTTGTGCAGGGAGACCCCTCTTC

Oy	61	PhaG1AspProCpeProCthArgrProSeArGrPoTpaAspApleProGluThGly	80
Db	244	TTTGAAAGATCTCCGCTACCGCCGCCAGTGTCCCTGGAAGACTGCTGGAACCTGGA	303
Oy	81	ValTTPProBProGluBProBraGrThArSpProProGInProProArGrProAspAspPro	100
Db	304	GTCAGGCCCCCTGAACCGGCTAGAAAGGATCTCTCAACTCCCGGGCTGAAGACCT	363
Oy	101	TTPProAlAGlyProGInProBProGluAsnProTTPProProAlaProGluValAspAsn	120
Db	364	TGGCCGAGAGAACCCAGGCCCCCAAAAAACCCCTGGCTCTCTGGCCCTGAGGTGGAAC	423
Oy	121	ArgProGInGluGluProAspLeuAspProProArGrGluGluIuYrArg	136
Db	424	CGACCTCAGAGAGCGAACCTTAACCCACCCGGGAGAGTACAGA	471

RESULT 2
ABN60006
ID ABN60006 standard; cDNA; 1473 BP.
...

AC ABN60006;

DT 28-JUN-2002 (first entry)

Novel human coding sequence SEQ ID NO: 417

KW Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;

KW neuroprotective; antiparkinsonian; protein therapy; EST; overexpressed

XX Homo sapiens
OS

AA WO20022660-A2
PN

PD 21-MAR-2002

10-SEP-2001: 2001WO-US026015.

PR 11-SEP-2000; 2000US-00659671.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;

2 XX
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841

DR P-PSDB; ABB97593.

PT An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis.

Claim 1; SEQ ID NO 417; 509pp; English

CC The present invention provides the protein and coding sequences of 444
CC novel human proteins. These were isolated from expressed sequences tags
CC (ESTs). They can be used to stimulate cell growth, to regulate
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC e.g. in burn treatment, to regulate the immune system e.g. to treat
CC multiple sclerosis, to regulate actin or inhibit e.g. to treat
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat strokes
CC and cancer, to screen for drugs, to treat inflammatory conditions e.g.
CC rheumatoid arthritis, and to treat nervous system disorders e.g.
CC Parkinson's disease. The present sequence is a coding sequence of the
CC invention

Sequence 1473 BP; 294 A; 491 C; 382 G; 306 T; 0 U; 0 Other;

Pred. No.:	1.01e-28	Length:	1473
Score:	808.00	Matches:	136
Percent Similarity:	100.00%	Conservative:	0

Best Local Similarity: 100.00% Mismatches: 0.
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-994-365-2 (1-136) x ABN60006 (1-1473)

Qy 1 MetileuabntrplysleuLeuGlyIleuValLeuCybleuHsthrArgGlyIle 20
 Db 636 ATGATCTCTCAAGTGAAGCTCTGGGATCTGTCTCTTGGCTGACACCCAGAGGCATC 695

Qy 21 SerGlySerGlyGlyHsIproSerHsIproProAlaGluHsPargGluAlaGlySer 40
 Db 696 TCAGGACGAGGAGGACCCCTCTCACCCACCCGAGAGGACGAGAGGAGGAGGCTCC 755

Qy 41 ProThrIeuProGlnGlyProProValProGlyAspProTrrProGlyAlaProProLeu 60
 Db 756 CCAACATGTCCTCAGGGGCCCCCGAGTCCCGTATACCTTGGCCAGAGGACCCCTCTC 815

Qy 61 PheGluAspProProProThrArgProSerArgProTrrPargAspLeuProGluThrGly 80
 Db 816 TTGGAGATCTCTCGCTTACCCGCCCAAGTCTCTCTGAGAGACCTGCTGAACACTGGA 875

Qy 81 ValTrrProProGluProProArgThrAspProProGlnProProArgProAspAspPro 100
 Db 876 GTCTGGCCCCCTGAACCGCTGAGAACGGATCTCTCAACCTCCCGGCTGACGACCT 935

Qy 101 TrrProAlaGlyProGlnProProGluAsnProTrrProProAlaProGluValAspAsn 120
 Db 936 TGCGCCGACAGACCCCGACCCCGAGAAACCCCTGGCTCTCTGCTGAGTGGACAC 995

Qy 121 ArgProGlnGluGluProAspLeuAspProProArgGluGlyTrrArg 136
 Db 996 CGACCTCAGAGAGGACCACTTGAACCCCGGAGAGTCAAGA 1043

RESULT 3
 ID ABK86967 standard; DNA; 2997 BP.
 AC ABK86967;
 XX
 XX
 DT 24-SEP-2002 (first entry)
 XX
 XX
 DE Human CAN-1 deletion polymorphism genomic DNA.
 XX
 KM Human; antipeoriatic; chromosome 6; candidate coding sequence-1; CAN-1;
 KM SBEK-1; STG; human leukocyte antigen C; HLA C; HLA Cw6; psoriasis; skin;
 KM keratinocyte; chronic inflammatory dermatosis; erythroderma; seborrheic;
 KM guttate; pustular variant; Reiter's disease; hyperproliferation;
 KM epidermis; differentiation; diagnosis; gene therapy; gene; de; SNP;
 KM single nucleotide polymorphism; deletion polymorphism.
 XX
 OS Homo sapiens.
 XX
 XX
 FH Key location/Qualifiers
 FT variation replace(11..12,CCAGA)
 FT /tag= a
 FT /note= "Deletion polymorphism"
 FT variation replace(114,T)
 FT /tag= b
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(351,A)
 FT /tag= c
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(550,A)
 FT /tag= d
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(956,G)
 FT /tag= e
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(1096,T)
 FT /tag= f
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(1196,A)

FT /tag= g
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(1390,T)
 FT /tag= h
 FT /standard_name= "Single nucleotide polymorphism"
 FT CDS 1481..2557
 FT /tag= i
 FT /product= "CAN-1"
 FT 1481..1535
 FT /tag= j
 FT /number= 1
 FT 1536..2201
 FT /tag= k
 FT /number= 1
 FT variation replace(1677,A)
 FT /tag= l
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(1875,T)
 FT /tag= m
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(1582,A)
 FT /tag= n
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(2016,C)
 FT /tag= o
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(2107,G)
 FT /tag= p
 FT /standard_name= "Single nucleotide polymorphism"
 FT exon 2202..2557
 FT /tag= q
 FT /number= 2
 FT variation replace(2393,T)
 FT /tag= r
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(2651,G)
 FT /tag= s
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(2818,G)
 FT /tag= t
 FT /standard_name= "Single nucleotide polymorphism"
 FT variation replace(2871,C)
 FT /tag= u
 FT /standard_name= "Single nucleotide polymorphism"

XX W0200244375-A2.
 XX
 XX 06-JUN-2002.
 XX
 XX 27-NOV-2001; 2001WC-US044506.
 XX
 XX 28-NOV-2000; 2000US-0253592P.
 XX 15-DEC-2000; 2000US-0256839P.
 XX
 XX (CELL-) CELLTech R & D INC.
 XX
 XX Charney P, Moss P, Mceuen M;
 XX
 XX WPI; 2002-508513/54.
 XX P-PSDB; AAU79579.
 XX
 XX Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation
 XX and differentiation, and polynucleotides encoding the polypeptide, useful
 XX for diagnosing or predicting susceptibility to psoriasis in individual.
 XX
 XX Example 3; Page 92-93; 95pp; English.
 XX
 XX The invention discloses isolated candidate coding sequence-1 (CAN-1),
 XX SBEK-1 (not defined) and STG (not defined) polypeptides, and the
 XX polynucleotides encoding them. All three genes were identified due to
 XX their proximity to the human leukocyte antigen C (HLA C) locus on
 XX chromosome 6. The HLA Cw6 allele is associated with psoriasis and as the
 XX three genes are expressed in normal skin and/or keratinocyte tissue, they

PI Charnley P, Moss P, Mceuen M;
XX
XX WPI: 2002-508513/54.
DR P-PSDB; AAU79579.

PT Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation
PT and differentiation, and polynucleotides encoding the polypeptide, useful
XX for diagnosing or predicting susceptibility to psoriasis in individual.
XX
PS Claim 18; Page 82-84; 95pp; English.

XX The invention discloses isolated candidate coding sequence-1 (CAN-1),
CC SEBK-1 (not defined) and STG (not defined) polypeptides, and the
CC polynucleotides encoding them. All three genes were identified due to
CC their proximity to the human leukocyte antigen C (HLA C) locus on
CC chromosome 6. The HLA Cw6 allele is associated with psoriasis and as the
CC three genes are expressed in normal skin and/or keratinocyte tissue, they
CC may also have a role in psoriasis. Psoriasis is a chronic inflammatory
CC dermatosis that is characterised by hyperproliferation of epidermal
CC cells. Possible treatments against psoriasis involve the inhibition of
CC movement of cells into the epidermis, or the inhibition of
CC hyperproliferation or abnormal differentiation of keratinocytes, by the
CC inhibition of the CAN-1, STG or SEBK-1 polypeptides binding to their
CC binding partners. The polypeptides are useful for diagnosing or
CC predicting the susceptibility to psoriasis in an individual, for
CC ameliorating the symptoms and/or progression of psoriasis and for
CC identifying agents useful for treating psoriasis or modulating the
CC activity of the polypeptide. The polypeptides are also useful for
CC enhancing the level of CAN-1, STG or SEBK-1 biological activity in a cell
CC or tissue. The nucleic acid molecules are useful as hybridisation probes
CC in diagnostic procedures (such as diagnosing the presence of psoriasis or
CC the propensity to develop psoriasis) and for suppressing the expression
CC of CAN-1 or STG gene (e.g. antisense inhibition, gene therapy).
CC Antisense, raised against the polypeptides, are useful for decreasing
CC the level of CAN-1, STG or SEBK-1 biological activity in a cell. The
CC sequence presented is the human candidate coding sequence-1 (CAN-1)
CC genomic DNA
XX

SO Sequence 3001 BP; 619 A; 786 C; 914 G; 682 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.05e-24	Length:	3001
Score:	712.00	Matches:	118
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	88.12%	Indels:	0
DB:	6	Gaps:	0

US-09-994-365-2 (1-136) x ABK86963 (1-3001)

QY 19 GYIIIESerGIYserGIYHIEProSerHIEProProaIaGIUaPaaGIGIUIaA 38
DB 2205 GGATCTCAGCAGCAGGAGGAGCCCTCTACCCAGCCAGAGGAGGAGGCA 2264
QY 39 GYIserProThIeupProGInGIYProProVaIaProGIYasPProTTPProGIYAlaPro 58
DB 2265 GGCTCCCAACATTCGCTCAGGGGCCCCCAGTCCCGGTACCTTGGCAGGGGCAACC 2224
QY 59 ProIeupheGIUaPProProProThIaPProSerIaPProTTPaPaaPleupProGIU 78
DB 2325 CCTCTTTTAAAGATCCTCGGCTTACCGCCCAAGTGTGCTCGAAGAGACCTGCTGAA 2384
QY 79 ThGIYValITrProProGIUProProaIThIaPProProGIUProProaITPProaP 98
DB 2385 ACTGGAGTCTGGCCCTGAAACGCTGAACGATCTCTCAACCTCCCGGCTGAC 2444
QY 99 AspProITrProaIaGIYProGInPProProGIUaPProTTPProProaIaPProGIUVal 118
DB 2445 GACCTTTGGCCGAGAGACCCAGCCCAAGAAACCTCGCTCTGCTGAGGTG 2504
QY 119 AspAaPaaPProGInGIUProaPleupProProaITPProGIUaPProGIUaP 136
DB 2505 GACAACGAGCCTCAGAGAGAGAGACCTAGACCAACCCCGGAGAGGTACAGA 2558

RESULT 5
AAH45310
ID AAH45310 standard; DNA: 25235 BP.

XX AC AAH45310;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human SEBK1 DNA.
XX
XX Human; MHC S; major histocompatibility complex S; vulgar psoriasis;
KW diagnosis; primer; SEBK1; HCR; a-helix coiled-coil rod homologue;
KW polymorphism; ds.
XX

OS	Key	Location/Qualifiers
XX	FT exon	1..420
XX	FT intron	421..1281
XX	FT exon	1282..1405
XX	FT intron	1406..1601
XX	FT exon	1602..1702
XX	FT intron	1703..2351
XX	FT exon	2352..2364
XX	FT intron	2365..6286
XX	FT exon	6287..6509
XX	FT intron	6510..10416
XX	FT exon	10417..10493
XX	FT intron	10494..14243
XX	FT exon	14244..14407
XX	FT intron	14408..14243
XX	FT exon	14244..25190
XX	FT exon	25191..25235
XX	FT exon	25236..

PN WO200142458-A1.

PD 14-JUN-2001.

XX 06-DEC-2000; 2000WO-JP008624.

XX 06-DEC-1999; 99JP-00346867.

XX (INOK/) INOKO H.

XX Inoko H, Tamiya G;

DR WPI; 2001-381680/40.

XX New primer DNA, useful for detecting vulgar psoriasis.

XX Claim 1; Page 46-62; 106pp; Japanese.

XX The invention relates to a method of diagnosing vulgar psoriasis using
CC primers based on the sequences of the human MHC S, SEBK1 and HCR genes.
CC By analysing the sequences of these genes in Japanese patients with
CC psoriasis and in normal subjects, it has been found that some of the
CC examined polymorphisms correlate significantly to the group of patients
CC with psoriasis. Vulgar psoriasis can therefore be diagnosed by analysing

CC these gene polymorphisms. The present sequence is the human SEEK1 gene
CC which was used to design primers for use in the invention
XX

Sequence 25235 BP; 5967 A; 6703 C; 6487 G; 6078 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	2,13e-23	25235	118	0	0	0
Percent Similarity:	712.00					
Best Local Similarity:	100.00%					
Query Match:	88.12%					

US-09-994-365-2 (1-136) x AAH45310 (1-25235)

QY	19	GLYIleSerGIySerGIuGIyHISProSerHISProProAlaGIuAspArgGIuGIuAla	38
DB	1754	GGCATCTCAGAGCGAGGGCCACCCCTCTACCCACCCGAGAGGAGGCA	1813
QY	39	GLySerProThrIeuProGIuGIyProGIuValProGIyAspProTTPProGIyAlaPro	58
DB	1814	GGCTCCCAACATGGCTCTCAGGGCCCCCAGTCCCGGTACCTTGGCCAGGGGCAACC	1873
QY	59	ProIeuPheGIuAspProProPProThArgProSerArgProTTPArgAspIeuProGIu	78
DB	1874	CTCTCTTGAAGATCCTCCGCTACCCGCCAGTGTCTCTGGAGAGACCTGCTGAA	1933
QY	79	ThGIyValTTPProProGIuPProPProArgThArgProProGIuPProPProArgProAsp	98
DB	1934	ACGGAGTCTGGGCCCCCTGAACCGCTGAACGGATCTCTCAACCTCCCGGCTGAC	1993
QY	99	AspProTTPProAlaGIyProGIuPProGIuAsnProTTPProProAlaProGIuVal	118
DB	1994	GACCTTGGCGGCGAGAGACCCCAAGCCCAAGAAACCCCTGGCTCTGCTGAGGTG	2053
QY	119	AspAsnArgProGIuGIuGIuPProAspIeuAspProProArgGIuGIuTyrArg	136
DB	2054	GACAAACGACCTCAGAGAGAGACGAGACCTAGACCCCGGAGAGATACAGA	2107

RESULT 6

ABQ75680 standard; DNA; 55050 BP.

XX	AC	ABQ75680;
XX	DT	11-NOV-2002 (first entry)
XX	DE	Human SEEK1 consensus genomic DNA.
XX	KM	Human; SEEK1; chromosome 6p21; inflammatory disease; antiinflammatory;
XX	KW	antipsoriatic; gene therapy; gene; ds.
XX	OS	Homo sapiens.
XX	PN	WO200264831-A2.
XX	PD	22-AUG-2002.
XX	PF	13-FEB-2002; 2002WO-GB000653.
XX	PR	13-FEB-2001; 2001GB-00003514.
XX	PA	(OXAG-) OXAGEN LTD.
XX	PI	Lench NJ, Allen MJ, Nicholls RK;
XX	DR	WPI; 2002-667013/71.
XX	PT	Polymorphisms in the SEEK1 gene and polynucleotides encoding the SEEK1
XX	PT	gene, for treating, diagnosing or determining susceptibility to SEEK1
XX	PT	mediated disease, e.g. inflammatory disease such as psoriasis.
XX	PS	Claim 4; Fig 2; 69pp; English.

XX The present invention describes a polynucleotide (I) comprising: (a) a
CC nucleic acid sequence (II) encoding the SEEK1 gene; or (b) a nucleic acid
CC sequence (III) encoding a fragment of the SEEK1 gene; or (c) a nucleic
CC acid sequence (IV) that hybridises under stringent conditions to the
CC polynucleotide of (II) or (III). (I) has antiinflammatory and
CC antipsoriatic activities and can be used in gene therapy. The alleles of
CC one or more polymorphisms in the SEEK1 gene can be used for the
CC manufacture of a medicament for the diagnosis and treatment of SEEK1
CC mediated disease. SEEK1 protein fragments are useful in diagnostic,
CC prognostic or therapeutic methods, or as research tools in drug
CC screening. Human SEEK1 is located to chromosome 6p21. The present
CC sequence represents a human SEEK1 nucleotide sequence

Sequence 55050 BP; 13076 A; 14198 C; 14560 G; 13197 T; 0 U; 19 Other;

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	3.92e-23	55050	118	0	0	0
Percent Similarity:	712.00					
Best Local Similarity:	100.00%					
Query Match:	88.12%					

US-09-994-365-2 (1-136) x ABQ75680 (1-55050)

QY	19	GLYIleSerGIySerGIuGIyHISProSerHISProProAlaGIuAspArgGIuGIuAla	38
DB	27099	GGCATCTCAGAGCGAGGGCCACCCCTCTACCCACCCGAGAGGAGGCA	27158
QY	39	GLySerProThrIeuProGIuGIyProGIuValProGIyAspProTTPProGIyAlaPro	58
DB	27159	GGCTCCCAACATGGCTCTCAGGGCCCCCAGTCCCGGTACCTTGGCCAGGGGCAACC	27218
QY	59	ProIeuPheGIuAspProProPProThArgProSerArgProTTPArgAspIeuProGIu	78
DB	27219	CTCTCTTGAAGATCCTCCGCTACCCGCCAGTGTCTCTGGAGAGACCTGCTGAA	27278
QY	79	ThGIyValTTPProProGIuPProPProArgThArgProProGIuPProPProArgProAsp	98
DB	27279	ACTGAGTCTGGCCCCCTGAACCGCTTGAACGGATCTCTCACTCCCGGCTGAC	27338
QY	99	AspProTTPProAlaGIyProGIuPProGIuAsnProTTPProProAlaProGIuVal	118
DB	27339	GACCTTGGCGGCGAGAGACCCCAAGAAACCCCTGGCTCTGCTGAGGTG	27398
QY	119	AspAsnArgProGIuGIuGIuPProAspIeuAspProProArgGIuGIuTyrArg	136
DB	27399	GACAAACGACCTCAGAGAGAGACGAGACCTAGACCCCGGAGAGATACAGA	27452

RESULT 7

ACH72505 standard; DNA; 565 BP.

XX	AC	ACH72505;
XX	DT	29-JUL-2004 (first entry)
XX	DE	Human genome derived single exon probe #5700.
XX	KM	Human; probe; ss; gene expression; single exon probe; microarray;
XX	KW	alternative splicing event; genomic alteration.
XX	OS	Homo sapiens.
XX	PN	US2003194704-A1.
XX	PD	16-OCT-2003.
XX	PF	03-APR-2002; 2002US-00029386.
XX	PR	03-APR-2002; 2002US-00029386.
XX	PS	

PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANK/) HANZEL D K.
 XX
 PI Penn SG, Rank DR, Hanzel DK;
 XX
 DR WPI; 2004-119264/12.
 XX
 PT New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.
 PT
 PS
 PS Claim 15; SEQ ID NO 5700; 80pp; English.
 XX
 CC The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridizes under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subsequence, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterizing
 CC alternative splicing events, in detecting and characterizing gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in printing the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docid=20030194704
 XX
 XX Sequence 565 BP; 99 A; 227 C; 112 G; 127 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Score: 2.03e-14 Length: 565
 Percent Similarity: 100.00% Matches: 79
 Percent Similarity: 100.00% Conserved: 0
 Percent Similarity: 100.00% Mismatches: 0
 Query Match: 60.15% Indels: 0
 DB: 12 Gaps: 0
 US-09-994-365-2 (1-136) x ACH72505 (1-565)
 QY 58 ProProLeuPheGluAaPProProProThraArgProSeArArgProTPaArgAaPLeuPro 77
 Db 1 CCCCCTCTCTTTGAAGAATCCCTCCGCTACCGCCCGCTGCTCCCTGAGAGACTCTCT 60
 QY 78 GluThrGlyValTyrPProProGluPProProArgThraArgPProPProGluInProProArgPro 97
 Db 61 GAAACCTGAGCTGGCCCTCCGAAACCGCTGAAACGAGATCTCTCTCAACCTCCCGGCT 120
 QY 98 AspAaPProTProAlaGlyPProGluInProProGluInPProTProProAlaPProGlu 117

Db 121 GACACCCCTTGCGGAGAGACCCAGCCCGCAAAAAACCTTGCCCTCTGCCCCCTAG 180
 QY 118 ValAspAaPProGluInGluPProAaPLeuAaPProProArgGluInPArg 136
 Db 181 GTGACACACCCACTTCAGAGAGCCAGACTTACCCACCCCGGAGAGTACAGA 237
 RESULT 8
 ACH86315
 ID ACH86315 standard; DNA; 157 BP.
 AC ACH86315;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human genome derived single exon probe #19510.
 XX
 KW Human; probe; sg; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.
 XX
 OS Homo sapiens.
 PN US2003194704-A1.
 XX
 PD 16-OCT-2003.
 XX
 PF 03-APR-2002; 2002US-00029386.
 XX
 PR 03-APR-2002; 2002US-00029386.
 XX
 PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANK/) HANZEL D K.
 XX
 PI Penn SG, Rank DR, Hanzel DK;
 XX
 DR WPI; 2004-119264/12.
 XX
 PT New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.
 PT
 PS
 PS Claim 1; SEQ ID NO 19510; 80pp; English.
 XX
 CC The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridizes under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subsequence, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterizing gross
 CC alterations in the genomic locus that includes their exon, in assessing

CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docid=20030194704
XX

SQ Sequence 157 BP; 38 A; 64 C; 38 G; 17 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.85e-07	Length:	157
Score:	314.00	Matches:	51
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	38.86%	Indels:	0
DB:	12	Gaps:	0

US-09-994-365-2 (1-136) x ACH86315 (1-157)

QY 86 PROProArgThraSPProProGlnProProArgProAspProTTPProAlaGlyPro 105

Db 2 CCGCCTTGAACGATCCTCTCAACCTCCCGGCTGACGACCTTGGCCGACGAGCC 61

QY 106 GlnProProGlnAsnProTTPProProAlaProGluValAspAsnArgProGlnGlu 125

Db 62 CAGCCCCAGAAAAACCCCTGCTGCTGCTGAGGTGACCAACGACCTCAGAGAG 121

QY 126 ProAspLeuAspProProArgGlnGluTyrArg 136

Db 122 CCAGACTTGAACCCACCCCGGAAAGTACAGA 154

RESULT 9

ACA43990/c
ID ACA43990 standard; DNA; 711 BP.

AC ACA43990;

DT 19-JUN-2003 (first entry)

DE Prokaryotic essential gene #25647.

KW Antisense; ds; prokaryotic essential gene; cell proliferation;

OS Pseudomonas putida.

PN WO200277183-A2.

PD 03-OCT-2002.

PF 21-MAR-2002; 2002WO-US009107.

PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948893.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

PA (ELIT-) ELITRA PHARM INC.

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Tirwick JD, Carr GJ, Yamamoto R, Foreyth RA, Xu HH;

PI WPI; 2003-029926/02.

PT New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

PS Claim 14, SEQ ID NO 31860; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the best compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 711 BP; 120 A; 161 C; 304 G; 126 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.264	Length:	711
Score:	199.00 <td>Matches:</td> <td>46</td>	Matches:	46
Percent Similarity:	44.95% <td>Conservative:</td> <td>3</td>	Conservative:	3
Best Local Similarity:	42.20% <td>Mismatches:</td> <td>42</td>	Mismatches:	42
Query Match:	24.63% <td>Indels:</td> <td>18</td>	Indels:	18
DB:	8 <td>Gaps:</td> <td>6</td>	Gaps:	6

US-09-994-365-2 (1-136) x ACA43990 (1-711)

QY 27 ProSerHisProProAlaGluAspArgGlnGluValSerProThrIeuProGlnGly 46

Db 446 CCGGCAATGGCCACACCG-----TCACCGCGCTGCGG---TGG 411

QY 47 ProProValPro---GlyAspProTTPProGlyAlaProProIeuIeuheGluAspProPro 65

Db 410 CCACCACTTCCGCTTCCGCCACATGACCAACCGCCGACCACTT-----CCACACCA 357

QY 66 ProThrArgProSerArgProTTPArgAspLeuProGluThrGlyValTTPProGlu 85

Db 356 CCGTGGCCACACACACCGCGCTTCCACACACCG-----TGGCACCGCCA 309

QY 86 ProProArgThraSP-----ProProGlnProProArgProAspAspProTTPPro 102

Db 308 CCGCGCTTCCACCAACCGGTGACCGCCACCGCGCTTCCACCGCACCGCGTGGCCA 249

QY 103 AlaGlyProGlnProProGluAsnProTTPProProAlaProGluValAspAsnArgPro 122

Db 248 CCGCGCGCGCGCTTCCACCGCACCGGTGACCGCGCGCGCTTCCACCGCACCG 189

QY 123 GlnGluGluProAspLeuAspProPro 131

Db 188 TGGCCACCGCCACCGCCACCGCCACCG 162

RESULT 10

ACA40420/c
ID ACA40420 standard; DNA; 2772 BP.

AC ACA40420;

XX

DT	19-JUN-2003	(first entry)
XX		
DE	Prokaryotic essential gene #22077.	
KW	Antisense; ds; prokaryotic essential gene; cell proliferation;	
KW	drug design; gene.	
XX		
OS	Mycobacterium tuberculosis.	
XX		
PN	WO200277183-A2.	
XX		
PD	03-OCT-2002.	
XX		
PF	21-MAR-2002; 2002WO-US009107.	
XX		
PR	21-MAR-2001; 2001US-00815242.	
PR	06-SEP-2001; 2001US-00948993.	
PR	25-OCT-2001; 2001US-0342923P.	
PR	08-FEB-2001; 2002US-00078851.	
PR	06-MAR-2002; 2002US-0362699P.	
XX		
PA	(ELITRA) ELITRA PHARM INC.	
XX		
PI	Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JW;	
PI	Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;	
XX		
DR	WPI: 2003-029926/02.	
XX	P-PSDB; ABU36550.	
PT	New antisense nucleic acids, useful for identifying proteins or screening	
PT	for homologous nucleic acids required for cellular proliferation to	
PT	isolate candidate molecules for rational drug discovery programs.	
XX		
PS	Claim 14; SEQ ID NO 28230; 1766bp; English.	
XX		
CC	The invention relates to an isolated nucleic acid comprising any one of	
CC	the 6213 antisense sequences given in the specification where expression	
CC	of the nucleic acid inhibits proliferation of a cell. Also included are:	
CC	(1) a vector comprising a promoter operably linked to the nucleic acid	
CC	encoding a polypeptide whose expression is inhibited by the antisense	
CC	nucleic acid; (2) a host cell containing the vector; (3) an isolated	
CC	polypeptide or its fragment whose expression is inhibited by the	
CC	antisense nucleic acid; (4) an antibody capable of specifically binding	
CC	the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular	
CC	proliferation or the activity of a gene in an operon required for	
CC	proliferation; (7) identifying a compound that influences the activity of	
CC	the gene product or that has an activity against a biological pathway	
CC	required for proliferation, or that inhibits cellular proliferation; (8)	
CC	identifying a gene required for cellular proliferation or the biological	
CC	pathway in which a proliferation-regulated gene or its gene product lies	
CC	or a gene on which the test compound that inhibits proliferation of an	
CC	organism acts; (9) manufacturing an antibiotic; (10) profiling a	
CC	compound's activity; (11) a culture comprising strains in which the gene	
CC	product is overexpressed or underexpressed; (12) determining the extent	
CC	to which each of the strains is present in a culture or collection of	
CC	strains; or (13) identifying the target of a compound that inhibits the	
CC	proliferation of an organism. The antisense nucleic acids are useful for	
CC	identifying proteins or screening for homologous nucleic acids required	
CC	for cellular proliferation to isolate candidate molecules for rational	
CC	drug discovery programs, or for screening homologous nucleic acids	
CC	required for proliferation in cells other than <i>S. aureus</i> , <i>S. typhimurium</i> ,	
CC	<i>K. pneumoniae</i> or <i>P. aeruginosa</i> . The present sequence is one of the target	
CC	prokaryotic essential genes. Note: The sequence data for this patent did	
CC	not form part of the printed specification, but was obtained in	
CC	electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences	
XX		
SQ	Sequence 2772 BP; 397 A; 904 C; 1108 G; 363 T; 0 U; 0 Other;	
Alignment Scores:		
Pred. No.:	0.805	Length: 2772
Score:	198.50	Matches: 51
Percent Similarity:	32.54%	Conservative: 4

[illegible]

WP	AA199682_26	260001	2710000
WP	AA199682_27	270001	2810000
WP	AA199682_28	280001	2910000
WP	AA199682_29	290001	3010000
WP	AA199682_30	300001	3110000
WP	AA199682_31	310001	3210000
WP	AA199682_32	320001	3310000
WP	AA199682_33	330001	3410000
WP	AA199682_34	340001	3510000
WP	AA199682_35	350001	3610000
WP	AA199682_36	360001	3710000
WP	AA199682_37	370001	3810000
WP	AA199682_38	380001	3910000
WP	AA199682_39	390001	4010000
WP	AA199682_40	400001	4110000
WP	AA199682_41	410001	4210000
WP	AA199682_42	420001	4310000
WP	AA199682_43	430001	4410000
WP	AA199682_44	440001	4511529

Pred. No.:	14.2	length:	110000
Score:	198.50	Matches:	51
Percent Similarity:	32.54%	Conservative:	4
Best Local Similarity:	30.18%	Mismatches:	45
Query Match:	24.57%	Indels:	69
DB:	4	Gaps:	6

US-09-994-365-2 (1-136) x AAI99682_10 (1-110000)

[illegible]

RESULT	12	
AA199683	10/c	
Continuation (11 of 44) of AA199683 from base 1000001 (Mycobacterium tuberculosis strain)		
WP	Sequence split into 44 fragments	LOCUS AA199683 Accession AA199683
WP	Fragment Name	Begin
AA199683_01		1
AA199683_01		110000
WP		End
AA199683_01		210000

WP	AAI199683	02	200001	310000
WP	AAI199683	03	200001	310000
WP	AAI199683	04	400001	510000
WP	AAI199683	05	500001	610000
WP	AAI199683	06	600001	710000
WP	AAI199683	07	700001	810000
WP	AAI199683	08	800001	910000
WP	AAI199683	09	900001	1010000
WP	AAI199683	10	1000001	11100000
WP	AAI199683	11	1100001	12100000
WP	AAI199683	12	1200001	13100000
WP	AAI199683	13	1300001	14100000
WP	AAI199683	14	1400001	15100000
WP	AAI199683	15	1500001	16100000
WP	AAI199683	16	1600001	17100000
WP	AAI199683	17	1700001	18100000
WP	AAI199683	18	1800001	19100000
WP	AAI199683	19	1900001	20100000
WP	AAI199683	20	2000001	21100000
WP	AAI199683	21	2100001	22100000
WP	AAI199683	22	2200001	23100000
WP	AAI199683	23	2300001	24100000
WP	AAI199683	24	2400001	25100000
WP	AAI199683	25	2500001	26100000
WP	AAI199683	26	2600001	27100000
WP	AAI199683	27	2700001	28100000
WP	AAI199683	28	2800001	29100000
WP	AAI199683	29	2900001	30100000
WP	AAI199683	30	3000001	31100000
WP	AAI199683	31	3100001	32100000
WP	AAI199683	32	3200001	33100000
WP	AAI199683	33	3300001	34100000
WP	AAI199683	34	3400001	35100000
WP	AAI199683	35	3500001	36100000
WP	AAI199683	36	3600001	37100000
WP	AAI199683	37	3700001	38100000
WP	AAI199683	38	3800001	39100000
WP	AAI199683	39	3900001	40100000
WP	AAI199683	40	4000001	41100000
WP	AAI199683	41	4100001	42100000
WP	AAI199683	42	4200001	43100000
WP	AAI199683	43	4300001	4403765

Alignment Scores:	
Pred. No.:	14.2
Score:	198.50
Percent Similarity:	32.54%
Best Local Similarity:	30.18%
Query Match:	24.57%
DB:	4
Length:	110000
Matches:	51
Conservative:	4
Mismatches:	45
Indels:	69
Gaps:	6

US-09-994-365-2 (1-136) X AAI99683_10 (1-110000)

QY	27	ProSerHisProProIalaGluAspArgGluAlaAGlySerProThrLeuProGlnSjly	46
Db	91482	CCGCCGATGGCGCCGCCGCCGCCTGGCCGCCGCCGCGCCTGGCCGCCGCCACAGCCG	914223
QY	47	ProProValaProGlyAspProTrpProGlyAlaProProleuPheGluAspPro-----	64
Db	91422	CCAATAACGCGCGCGCGCGCGCTGGCGCGTGGCCGCCCGTGCCCAACCCGACCTTTGGCTG	91363
QY	65	-----ProBraThraArgProSerArg	71
Db	91362	CGCGCGATCCACCCGCGGAACCAACCGAATCCGCGCGCGCGCGCGCGCTCCCCGTGGCCG	91303
QY	72	ProTrp-----ArgAspLeuPro	77
Db	91302	CCTCTGGCGCGCTGTCACACAATAGCGAGACGTAATGCCCTCAGCGGCGCACGCGATTGCCG	91243
QY	78	GluThrGlyValTrpProProGluProProAlaGlyThrAsp-----	90
Db	91242	CGAGCACGCGCTGGCGCACCATGCGCGCGGTACGCCCATCGCCGTGATATCCCCCGTGG	91183

```

Qy 91 -----ProProGlnPro 94
Db 91182 CCGAACAACGCCGAGCCGTGGCCGCCGACCCCGCCGCCGCGATGCCGATGCCG 91123
Qy 95 ProArgProAspAspProTTPProAlaGly-----104
Db 91122 CCGATGCCCGCGGTGCGG---CCGCGGAGCCGCGACCATGCCGCGCCCGCCGTC 91066
Qy 105 -----ProGlnProGluAsnProTTPProAlaProGluValAspAsnArg 121
Db 91065 CCGGAGCCCCCAAGTCCGCGCGAGCCACCTGGCGCGCGACCAACCGTTG-----91015
Qy 122 ProGlnGluGluProAspLeuAspPro 130
Db 91014 CCGAATAGCAGCCGCGCTTGGCCGCCG 90988

RESULT 13
AA123276/c
ID AA123276 standard; DNA; 446 BP.
AC AA123276;
XX
XX 12-OCT-2001 (first entry)
DT
DE Probe #13209 for gene expression analysis in human cervical cell sample.
XX
XX Probe: human; microarray; gene expression; cervical epithelial cell;
XX
XX Homo sapiens.
XX
XX WO200157278-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000670.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX
XX (MOLF-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488901/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX
XX gene expression in human cervical epithelial cells.
XX
XX Claim 25; SEQ ID NO 13209; 487bp; English.
XX
XX The present invention relates to human single exon nucleic acid probes
XX
XX (SENPs). The present sequence is one such probe. The SENPs are derived
XX
XX from human Hela cells. The SENPs can be used to produce a single exon
XX
XX microarray, which can be used for measuring human gene expression in a
XX
XX sample derived from human cervical epithelial cells. By measuring gene
XX
XX expression, the probes are therefore useful in grading and/or staging of
XX
XX diseases of the cervix, notably cervical cancer. Note: The sequence data
XX
XX for this patent did not form part of the printed specification, but was
XX
XX obtained in electronic format directly from WIPO at
XX
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 446 BP; 31 A; 26 C; 254 G; 135 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX
XX Pred. No.: 0.265 Length: 446
XX
XX Score: 195.50 Matches: 46
XX
XX Percent Similarity: 40.32% Conservative: 4
XX

```

```

Best Local Similarity: 37.10% Mismatches: 64
Query Match: 24.20% Indels: 10
DB: 4 Gaps: 2
US-09-994-365-2 (1-136) x AA123276 (1-446)
Qy 14 CysLeuHisThrArg-GlyIleSerGlySerGluGlyHisProSerHisProProAlaG1 33
Db 443 TGCACGACAGCAAAATATATCATCTGCACACCAACCAACCAACCAACCAACCAATC 384
Qy 33 uAspArgGluGluAlaGlySerProThrLeuProGlnGlyProProValProGlyAspPr 53
Db 383 ACCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 324
Qy 53 oTTPProGlyAlaProProLeuPheGluAspProProProTTPArgProSerArgProTr 73
Db 323 ACCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 264
Qy 73 pArgAspLeuProGluThrGlyValTTPProProGluProProArgThrAspProG1 93
Db 263 ACCATCATCACCA-----CCACCACCAACCAACCAACCAACCAACCAACCA 216
Qy 93 nProProArgProAspAspProTTPProAlaGlyProGlnProProGluAsnProTTPPr 113
Db 215 ACCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 156
Qy 113 o-----ProAlaProGluValAspAsnArgProGlnGluGluProAspLe 128
Db 155 ATCATCATCACCAATCACCGGCACCATCATCATCACCAACCAACCGCGCCACCA 96
Qy 128 uAspProPro 131
Db 95 GCCACCGCCA 86

RESULT 14
ABA68382/c
ID ABA68382 standard; DNA; 446 BP.
XX
XX ABA68382;
XX
XX 01-FEB-2002 (first entry)
DT
DE Human foetal liver single exon nucleic acid probe #16687.
XX
XX Human foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
XX Homo sapiens.
XX
XX WO200157277-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000669.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX
XX (MOLF-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX
XX gene expression in human foetal liver.
XX
XX Claim 4; SEQ ID NO 16687; 639bp + Sequence Listing; English.
XX

```

CC The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and/or
CC displaying gene expression in samples derived from human foetal liver. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

Sequence 446 BP; 31 A; 26 C; 254 G; 135 T; 0 U; 0 Other;

Alignment Scores:	
Pred. No.:	0.265
Score:	195.50
Percent Similarity:	40.32%
Best Local Similarity:	37.10%
Query Match:	24.20%
DB:	4
	2
Length:	446
Matches:	46
Conservative:	4
Mismatches:	64
Indels:	10
Gaps:	2

US-09-994-365-2 (1-136) X ABA68382 (1-446)

Qy	1	CysLeuHisThrArg-GlyIleSerIylSerGluHisProSerHisProProAlaG1	33
Db	443	TGCACGCACGCGAAATATATCTACTCTACCCACCACCACCACCACCAACCAACCAACCAATC	38
Qy	33	uasPargIuGluaIaGlySerProThrIeuProGluInglProProValProGlyasPpr	53
Db	383	ACCACGACGACGACGACGACATTCACGACGACGACGACGACGACGACGACGACGACGACGAC	32
Qy	53	oTTPProGlyAlaProProIeuPheGluasPprProProProThrArgProSerArgProTr	73
Db	323	ACCACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC	26
Qy	73	pArgAspIeuProGluIuThrGlyValIrrProProGluPupProArgThrAspProProG1	93
Db	263	ACCATATATCCACCA-----CCACGACGACGACGACGACGACGACGACGACGACGACGAC	216
Qy	93	nProProArgProAspAspProTrTPProAlaGlyProGluIngluPuaenProTrPr	113
Db	215	ACCACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC	156
Qy	113	o-----ProAlaProGluValIasPasnArgProGluIngluPupProAspIe	128
Db	155	ATCATCAGCACCATTCACGCGACGACGACGACGACGACGACGACGACGACGACGACGAC	96
Qy	128	uasPprPro	131
Db	95	GCCACGCGCA	86

RESULT 15

ID AAI48596 standard; DNA; 446 BP.

AC AAI48596;

DT 17-OCT-2001 (first entry)

DE Probe #17282 used to measure gene expression in human placenta sample.

KM Probe; microarray; human; placenta; antenatal diagnosis;
KM genetic disorder; BS.

OS Homo sapiens.

PN W0200157272-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000663.

PR 04-FEB-2000; 2000US-0180312P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366
PR 21-SEP-2000; 2000US-0234687P
PR 27-SEP-2000; 2000US-0236359P
PR 04-OCT-2000; 2000GB-00024263

PA (MOLE-) MOLECULAR DYNAMICS IN

PI Penn SG, Hanzel DK, Chen W,

DR WPI; 2001-488897/53.

PT Human genome-derived single exc

XX

XX

CC The present sequence is one such probe. The probes are useful for

CC expression in samples derived from

XX

Pred. No.:	0.265	Length:	446
------------	-------	---------	-----

Percent Similarity: 40.32% Conservative: 4

Query Match:	24.20%	Indels:	10
		Calls:	9

[illegible]

Q. 1. The following are the names of the members of the committee. Write the names in the order in which they were mentioned in the text.

[illegible]

Search completed: January 11, 2005, 12:04:34
Job time : 477.936 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 11, 2005, 08:16:10 ; Search time 4026 Seconds
(without alignments)
10465.753 Million cell updates/sec

Title: US-09-994-365-1

Perfect score: 891
Sequence: 1 cccctcgsgggtcccgagca.....taaaatcatgtttctta 891

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

GenBml: *
1: gb_ba: *
2: gb_beg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_str: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	891	100.0	891	6	AX477387 Sequence
2	840	94.3	1143	6	CO722444 Sequence
3	840	94.3	1185	9	AF484420 Homo sapi
4	828	92.9	1473	6	AX406002 Sequence
5	781	87.7	1143	9	AB031480 Homo sapi
6	775	87.0	2997	6	AX477396 Sequence
7	775	87.0	3001	6	AX477390 Sequence
8	775	87.0	40878	9	AC004195 Homo sapi
9	728	81.7	113388	9	AL773544 Human DNA
10	724	81.3	25235	6	BD095297 The metho
11	724	81.3	30911	9	AB088114 Homo sapi
12	724	81.3	39196	9	AB023060 Homo sapi
13	724	81.3	55050	6	AX522117 Sequence
14	724	81.3	70288	9	AL662867 Human DNA
15	724	81.3	99999	9	AP000510 Homo sapi
16	724	81.3	135396	9	EX927139 Human DNA
17	622	69.8	204298	9	AL662844 Human DNA
18	269	30.2	300050	9	AB100083 Pan trogl
19	119	13.4	168887	9	AL662833 Human DNA

C 20	117	13.1	175689	9	AC148703	AC148703 Macaca mu
C 21	94	10.5	200068	9	AC148691	AC148691 Macaca mu
C 22	87	9.8	248	6	AR418279	AR418279 Sequence
C 23	87	9.8	248	6	AX978973	AX978973 Sequence
C 24	87	9.8	248	6	BD113832	BD113832 EST and e
C 25	60	6.7	60	6	CQ535442	CQ535442 Sequence
C 26	54	6.1	388	9	HS14A35	U18174 Human HLA c
C 27	41	4.6	306	9	HS14A32	U18171 Human HLA c
C 28	38	4.3	773	10	AF159091	AF159091 Mus muscu
C 29	38	4.3	809	10	AF484421	AF484421 Mus muscu
C 30	38	4.3	1377	10	AF159090	AF159090 Mus muscu
C 31	38	4.3	159179	10	MMHC322F16	AF111103 Mouse maj
C 32	38	4.3	226594	10	AC087216	AC087216 Mus muscu
C 33	33	3.7	250	9	HS14A26	U18163 Human HLA c
C 34	33	3.7	349980	6	AX344554	AX344554 Sequence
C 35	28	3.1	343	9	HS14A31	U18170 Human HLA c
C 36	26	2.9	204	6	AX911909	AX911909 Sequence
C 37	26	2.9	204	6	BD047442	BD047442 Sequence
C 38	26	2.9	383	4	AF484422	AF484422 Sus scrofa
C 39	26	2.9	154749	4	AB113354	AB113354 Sus scrofa
C 40	22	2.5	147524	2	AC069201	AC069201 Homo sapi
C 41	22	2.5	159479	2	AC074352	AC074352 Homo sapi
C 42	22	2.5	159705	2	AC092928	AC092928 Homo sapi
C 43	22	2.5	160042	2	AL365211	AL365211 Homo sapi
C 44	22	2.5	167152	9	AC092939	AC092939 Homo sapi
C 45	22	2.5	175968	9	AC018684	AC018684 Homo sapi

ALIGNMENTS

RESULT 1	AX477387	Sequence 1 from Patent WO0244375.	891 bp	DNA	linear	PAT 12-AUG-2002
LOCUS	AX477387					
DEFINITION	Sequence 1 from Patent WO0244375.					
ACCESSION	AX477387					
VERSION	AX477387.1	GI:22216617				
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens (human)					
	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					

REFERENCE	1	Charmley, P., Moss, P. and Mceuen, M.
AUTHORS		
TITLE		Compositions and methods for diagnosing or treating psoriasis
JOURNAL		Patent: WO 0244375-A1 06-JUN-2002;
CELL		Celltech R & D, Inc. (US)
FEATURES		Location/Qualifiers
source		1..891

CDS

/organism="Homo sapiens"	
/mol_type="unassigned DNA"	
/db_xref="taxon:9606"	
64..474	
/note="unassigned protein product"	
/codon_start=1	
/protein_id="CAD3680.1"	
/db_xref="GI:22216618"	
/translation="MILNMLGLILVCLHTRGISGSRGHPSPADREAGPTLP	
QGPVPGDPWGPAPLFEEDPPRPSRPMWDLDEPTGVWPPSPPTDPPQPPRDPWP	
AGQPPEPMPAPPEVNDPRQEBDDLPPEEYR"	

ORIGIN

Query Match	100.0%;	Score 891;	DB 6;	Length 891;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches	891;	Conservative 0;	Mismatches 0;	Indels 0;
		Gaps 0;		
Qy	1	CCCTCTGGGGTTCACGAGCAGCCAGCCAGCCAGCCAGCTTTGGGGCCAGTACATA	60	
Db	1	CCCTTTGGGGTTCACGAGCAGCCAGCCAGCCAGCCAGCTTTGGGGCCAGTACATA	60	
Qy	61	GCCATGATCTCTCACTGGAAGCTCTGGGAGTCTGTCTCTTGGCTGCACACCAAGGC	120	
Db	61	GCCATGATCTCTCACTGGAAGCTCTGGGAGTCTGTCTCTTGGCTGCACACCAAGGC	120	

QY 121 ATCTCAGGACGAGGCGCAACCCCTCTCAACCCGAGAGAGACCGAGAGGAGGCGAGGC 180
 DB 121 ATCTCAGGACGAGGCGCAACCCCTCTCAACCCGAGAGAGACCGAGAGGAGGCGAGGC 180
 QY 181 TCCCGAATTTGCTCTCAGGCGCCCGCCAGTCCCGGTGACCTTTGGCGAGGCGAGCCCT 240
 DB 181 TCCCGAATTTGCTCTCAGGCGCCCGCCAGTCCCGGTGACCTTTGGCGAGGCGAGCCCT 240
 QY 241 CTCTTAAAGATCTCTCGGCTCAACCGGCGGAGTCCCTGGAAGAGCTGGCTGAAGT 300
 DB 241 CTCTTAAAGATCTCTCGGCTCAACCGGCGGAGTCCCTGGAAGAGCTGGCTGAAGT 300
 QY 301 GGAATCTGAGCCCTCTGAGACCGCTCAGAAAGAGATCTCTCAACTCCCGGCGCTGAGAC 360
 DB 301 GGAATCTGAGCCCTCTGAGACCGCTCAGAAAGAGATCTCTCAACTCCCGGCGCTGAGAC 360
 QY 361 CTTTGGCCGCGAGAGACCGCCAGCCCGGAGAAACCTTGGCTCTCTGCGCTTGAAGT 420
 DB 361 CTTTGGCCGCGAGAGACCGCCAGCCCGGAGAAACCTTGGCTCTCTGCGCTTGAAGT 420
 QY 421 AACGACCTCAG 480
 DB 421 AACGACCTCAG 480
 QY 481 CCGCTCAGCGGTTCTGTCTCCAGGATCTCCAGGACCGACCGCTCTCAACTCTGAT 540
 DB 481 CCGCTCAGCGGTTCTGTCTCCAGGATCTCCAGGACCGACCGCTCTCAACTCTGAT 540
 QY 541 TCCCGTGAATCTTCCCAATTTAGCCTATCTCTTAAACCTCTTCTCAATCTCTGAT 600
 DB 541 TCCCGTGAATCTTCCCAATTTAGCCTATCTCTTAAACCTCTTCTCAATCTCTGAT 600
 QY 601 TTTATTTGAAACCGGTAAAGGTGTCTCAATTTCTGCTCCCTCTGAGATCCATA 660
 DB 601 TTTATTTGAAACCGGTAAAGGTGTCTCAATTTCTGCTCCCTCTGAGATCCATA 660
 QY 661 CTTAGTCTCAATCGCCGCTTTTCTCTGACAGCTTAAAGCTCTCTCAACTCTGAT 720
 DB 661 CTTAGTCTCAATCGCCGCTTTTCTCTGACAGCTTAAAGCTCTCTCAACTCTGAT 720
 QY 721 CTCAGGCGCTCGGCGCCCACTTCTCCACCGCGGTCTTCTGCGCGCGGATGCTGGG 780
 DB 721 CTCAGGCGCTCGGCGCCCACTTCTCCACCGCGGTCTTCTGCGCGCGGATGCTGGG 780
 QY 781 CAGGCGATGATCTGTGTCTCTTCTGCAACCGGTGAGGCGCGGAGAGATGAT 840
 DB 781 CAGGCGATGATCTGTGTCTCTTCTGCAACCGGTGAGGCGCGGAGAGATGAT 840
 QY 841 AGACAGCTGTCTCTTCCATGAAACGAAAAATTAATCATGTTTCTTAA 891
 DB 841 AGACAGCTGTCTCTTCCATGAAACGAAAAATTAATCATGTTTCTTAA 891

RESULT 2
 CQ722444 1143 bp DNA linear PAT 03-FEB-2004
 LOCUS Sequence 8378 from Patent WO02068579.
 DEFINITION CQ722444
 ACCESSION CQ722444
 VERSION CQ722444.1 GI:42283301
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
 TITLE Kites, such as nucleic acid arrays, comprising a majority of
 humamexons or transcripts, for detecting expression and other uses
 thereof
 JOURNAL Patent: WO 02068579-A 8378 06-SRP-2002;
 FEATUES PB Corporation (NY) (US)
 Location/Qualifiers

source 1..1143
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 94.3%; Score 840; DB 6; Length 1143;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 890; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ORIGIN

QY 1 CTCTTGGGGTTCCAGGACCCCAAGTCAAGCCCAAGCTTTGGGGGCGATACATA 60
 DB 253 CTCTTGGGGTTCCAGGACCCCAAGTCAAGCCCAAGCTTTGGGGGCGATACATA 312
 QY 61 GCCATGATCTCAACTGGAAGCTCTGAGGAGTCTGAGTCTTTGCTGACACAGAGGC 120
 DB 313 GCCATGATCTCAACTGGAAGCTCTGAGGAGTCTGAGTCTTTGCTGACACAGAGGC 372
 QY 121 ATCTCAGGACGAGGCGCAACCCCTCTCAACCCGAGAGAGACCGAGAGGCGAGGC 180
 DB 373 ATCTCAGGACGAGGCGCAACCCCTCTCAACCCGAGAGAGACCGAGAGGCGAGGC 432
 QY 181 TCCCGAATTTGCTCTCAGGCGCCCGCCAGTCCCGGTGACCTTTGGCGAGGCGAGCCCT 240
 DB 433 TCCCGAATTTGCTCTCAGGCGCCCGCCAGTCCCGGTGACCTTTGGCGAGGCGAGCCCT 492
 QY 241 CTCTTAAAGATCTCTCGGCTCAACCGGCGGAGTCCCTGGAAGAGAGCTGCTGAAGT 300
 DB 493 CTCTTAAAGATCTCTCGGCTCAACCGGCGGAGTCCCTGGAAGAGAGCTGCTGAAGT 552
 QY 301 GGAATCTGAGCCCTCTGAGACCGCTCAGAAAGAGATCTCTCAACTCCCGGCGCTGAGAC 360
 DB 553 GGAATCTGAGCCCTCTGAGACCGCTCAGAAAGAGATCTCTCAACTCCCGGCGCTGAGAC 612
 QY 361 CTTTGGCCGCGAGAGACCGCCAGCCCGGAGAAACCTTGGCTCTCTGCGCTTGAAGT 420
 DB 613 CTTTGGCCGCGAGAGACCGCCAGCCCGGAGAAACCTTGGCTCTCTGCGCTTGAAGT 672
 QY 421 AACGACCTCAG 480
 DB 673 AACGACCTCAG 732
 QY 481 CCGCTCAGCGGTTCTGTCTCCAGGATCTCCAGGACCGACCGCTCTCAACTCTGAT 540
 DB 733 CCGCTCAGCGGTTCTGTCTCCAGGATCTCCAGGACCGACCGCTCTCAACTCTGAT 792
 QY 541 TCCCGTGAATCTTCCCAATTTAGCCTATCTCTTAAACCTCTTCTCAATCTCTGAT 600
 DB 793 TCCCGTGAATCTTCCCAATTTAGCCTATCTCTTAAACCTCTTCTCAATCTCTGAT 852
 QY 601 TTTATTTGAAACCGGTAAAGGTGTCTCAATTTCTGCTCCCTCTGAGATCCATA 660
 DB 853 TTTATTTGAAACCGGTAAAGGTGTCTCAATTTCTGCTCCCTCTGAGATCCATA 912
 QY 661 CTTAGTCTCAATCGCCGCTTTTCTCTGACAGCTTAAAGCTCTCTCAACTCTGAT 720
 DB 913 CTTAGTCTCAATCGCCGCTTTTCTCTGACAGCTTAAAGCTCTCTCAACTCTGAT 972
 QY 721 CTCAGGCGCTCGGCGCCCACTTCTCCACCGCGGTCTTCTGCGCGCGGATGCTGGG 780
 DB 973 CTCAGGCGCTCGGCGCCCACTTCTCCACCGCGGTCTTCTGCGCGCGGATGCTGGG 1032
 QY 781 CAGGCGATGATCTGTGTCTCTTCTGCAACCGGTGAGGCGCGGAGAGATGAT 840
 DB 1033 CAGGCGATGATCTGTGTCTCTTCTGCAACCGGTGAGGCGCGGAGAGATGAT 1092
 QY 841 AGACAGCTGTCTCTTCCATGAAACGAAAAATTAATCATGTTTCTTAA 891
 DB 1093 AGACAGCTGTCTCTTCCATGAAACGAAAAATTAATCATGTTTCTTAA 1143

RESULT 3
 AF484420

LOCUS AF484420 1185 bp mRNA linear PRI 02-MAR-2003
DEFINITION Homo sapiens psoriasis susceptibility 1 candidate 2 (PSORS1C2)
ACCESSION AF484420
VERSION AF484420.1 GI:28628834
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1185)
Holm,S.J., O'Brien,K.P., Carlen,L. and Stahle-Backdahl,M.
The PSORS1C1 and PSORS1C2 genes in 6p21.3 associate strongly with
psoriasis in the Swedish population
JOURNAL Unpublished
2 (bases 1 to 1185)
Holm,S.J., O'Brien,K.P., Carlen,L. and Stahle-Backdahl,M.
Direct Submission
AUTHORS Submitted (15-FEB-2002) Dermatology, Karolinska Institute, L8:02
JOURNAL Karolinska Sjukhuset, Stockholm S-17176, Sweden
FEATURES
source
1..1185
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
/cfeature_type="skin"
1..1185
/gene="PSORS1C2"
325..735
/gene="PSORS1C2"
/codon_start=1
/product="psoriasis susceptibility 1 candidate 2"
/protein_id="AA049377.1"
/db_xref="GI:28628835"
/translation="MILNWKILGILVLCILHTRGISGSEGHSPHAPDRERAGSTLP
QGPPVDPMPGAPPLFEDPPRPSRPMDLPETGWPPEPRPTDPPQPRDPPMP
AGPPENPMPAPBVDNRPQEBDDLPREBRV"
ORIGIN
Query Match 94.3%; Score 840; DB 9; Length 1185;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 890; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCTTTGGGGTCCAGGCACTCAAGCTCAAGCCCACTTTGGGGCCAGTACATA 60
DB 262 CCTTTGGGGTCCAGGCACTCAAGCTCAAGCCCACTTTGGGGCCAGTACATA 321
QY 61 GCCATGATCCCTCACTGGAAGCTCTGGGGGATCCGTCCTTTGCTGCACACAGAGGC 120
DB 322 GCCATGATCCCTCACTGGAAGCTCTGGGGGATCCGTCCTTTGCTGCACACAGAGGC 381
QY 121 ATCTCAGGCAAGGAGGCACTCTCACTCACTCACTCACTCACTCACTCACTCACTCA 180
DB 382 ATCTCAGGCAAGGAGGCACTCTCTTACCACTCACTCACTCACTCACTCACTCACT 441
QY 181 TCCCAACATTGCTCTCAGGGCCCCCAGTCCCGGTGACCTTTGACGAGGCAACCCCT 240
DB 442 TCCCAACATTGCTCTCAGGGCCCCCAGTCCCGGTGACCTTTGACGAGGCAACCCCT 501
QY 241 CTCTTTAAGATCTCTCGGCTCAAGCCGCCAGTGTCTCTGGAAGACCTGCGTGAAGT 300
DB 502 CTCTTTAAGATCTCTCGGCTCAAGCCGCCAGTGTCTCTGGAAGACCTGCGTGAAGT 561
QY 301 GGAATCTGAGCCCTGGAACCGCTGGAACGATCTCTCACTCTCCCGGCTGAGGAC 360
DB 562 GGAATCTGAGCCCTGGAACCGCTGGAACGATCTCTCACTCTCCCGGCTGAGGAC 621
QY 361 CTTTGGCCGAGAGACCCCAAGCCCAAGAAAACCTTGGCTCTGCGCCCTGAGTGGAC 420
DB 622 CTTTGGCCGAGAGACCCCAAGCCCAAGAAAACCTTGGCTCTGCGCCCTGAGTGGAC 681

QY 421 AACGACCTCAGAGAGAGCAAGCTTAGACCAACCCCGGAGAGATACAGTAATGAGT 480
DB 682 AACGACCTCAGAGAGAGCAAGCTTAGACCAACCCCGGAGAGATACAGTAATGAGT 741
QY 481 CCCTCAGCGGTTTGTTCAGGCACTCTCAGGCAACCCAGCCCTCTCAGCCCTTGAT 540
DB 742 CCCTCAGCGGTTTGTTCAGGCACTCTCAGGCAACCCAGCCCTCTCAGCCCTTGAT 801
QY 541 TCCCGGAATCTTCCCAATTTAGCTATCTCTTAAACCTCTTCCTCAATCCCTGGT 600
DB 802 TCCCGGAATCTTCCCAATTTAGCTATCTCTTAAACCTCTTCCTCAATCCCTGGT 861
QY 601 TTTATCTGAACCCGTAAGGTGTGTCTCAATATTTCTGTCCTCTCAGATCCATA 660
DB 862 TTTATCTGAACCCGTAAGGTGTGTCTCAATATTTCTGTCCTCTCAGATCCATA 921
QY 661 CTATGCTCAATCGCCCGCTTTTCTCTGACAGCTTAAGCTACTCTCTACCTGCC 720
DB 922 CTATGCTCAATCGCCCGCTTTTCTCTGACAGCTTAAGCTACTCTCTACCTGCC 981
QY 721 CTCAGGCTCGGCCCACTACTCCACCCCGCTTCTCGCCGCGGCGATGCTGGGG 780
DB 982 CTCAGGCTCGGCCCACTACTCCACCCCGCTTCTCGCCGCGGCGATGCTGGGG 1041
QY 781 CAGGCTATGATCTGTGTTCCCTTCTGCACTGTGTGCGCGGCGAGAACTATCAGT 840
DB 1042 CAGGCTATGATCTGTGTTCCCTTCTGCACTGTGTGCGCGGCGAGAACTATCAGT 1101
QY 841 AGACAGCTGCTCTTCATGAAACGAAAAATATATATGTTTCTTAA 891
DB 1102 AGACAGCTGCTCTTCATGAAACGAAAAATATATATGTTTCTTAA 1152
RESULT 4
AX406002 1473 bp DNA linear PAT 14-JUN-2002
LOCUS Sequence 417 from Patent WO0222660.
DEFINITION AX406002
ACCESSION AX406002
VERSION AX406002.1 GI:21439443
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
Tang,Y.T., Liu,C., Zhou,P., Asundi,V., Zhang,J., Zhao,Q.A., Ren,F.,
Xue,A.J., Yang,Y., Weinman,T. and Drmanac,R.T.
Novel nucleic acids and polypeptides
Patent: WO 0222660-A 417 21-MAR-2002;
HSEQ, INC. (US)
FEATURES
source
1..1473
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
636..1046
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD35109.1"
/db_xref="GI:21439444"
/translation="MILNWKILGILVLCILHTRGISGSEGHSPHAPDRERAGSTLP
QGPPVDPMPGAPPLFEDPPRPSRPMDLPETGWPPEPRPTDPPQPRDPPMP
AGPPENPMPAPBVDNRPQEBDDLPREBRV"
ORIGIN
Query Match 92.9%; Score 828; DB 6; Length 1473;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 876; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 13 CCGAGGACCCCAAGCTCAGGCTCAAGCTTTGGGGGCAAGTACATAGCATGATCTTC 72
DB 585 CCGAGGACCCCAAGCTCAGGCTCAAGCTTTGGGGGCAAGTACATAGCATGATCTTC 644

```

QY 73 AACTGAAGCTCTGGGGATCTGCTCTTGTCTGTGACACACAGAGCATCTCAGCAGC 132
DB 645 AACTGGAAGCTCTGGGGATCTGCTCTTGTCTGTGACACACAGAGCATCTCAGCAGC 704
QY 133 GAGGGCCACCTCTTCAACCCACCCGACAGAGACCGAGAGAGGAGGCTCTCCCAACTTG 192
DB 705 GAGGGCCACCTCTTCAACCCACCCGACAGAGACCGAGAGAGGAGGCTCTCCCAACTTG 764
QY 193 CCTGAGGGCCCGCCAGTCCCGGATGACCTCTGGCAGAGGGACCCCTCTTTGAAGAT 252
DB 765 CCTGAGGGCCCGCCAGTCCCGGATGACCTCTGGCAGAGGGACCCCTCTTTGAAGAT 824
QY 253 CCTCGGCTACCCGCGCCAGTCTGCTCTGAGAGACCTGTCTGAACCTGAGTCTGCGCC 312
DB 825 CCTCGGCTACCCGCGCCAGTCTGCTCTGAGAGACCTGTCTGAACCTGAGTCTGCGCC 884
QY 313 CCTGAACCGCTTGAAGAGATCTCTCTACCTCTCCCGGCTTGAACCTTGGCCGCA 372
DB 885 CCTGAACCGCTTGAAGAGATCTCTCTACCTCTCCCGGCTTGAACCTTGGCCGCA 944
QY 373 GGAGCCGAGCCCGCAGAAAACCCCTGGCTCTGCGCCCTGAGGTGACCAACGACCTCAG 432
DB 945 GGAGCCGAGCCCGCAGAAAACCCCTGGCTCTGCGCCCTGAGGTGACCAACGACCTCAG 1004
QY 433 GAGAGCCAGACCTTGAACCCACCCCGGAGAGATGATATGAGTCTCCCTCAGCCGT 492
DB 1005 GAGAGCCAGACCTTGAACCCACCCCGGAGAGATGATATGAGTCTCCCTCAGCCGT 1064
QY 493 TCTGTCTCCAGGATCTTCAAGGACCCACGCTCTTCAACCTTGAATCTCCCTGATAT 552
DB 1065 TCTGTCTCCAGGATCTTCAAGGACCCACGCTCTTCAACCTTGAATCTCCCTGATAT 1124
QY 553 CTTCCTCAATTAAGCTATCTCTTAAACCTCTTCTCAATCTCCCTGATATCTGTAAC 612
DB 1125 CTTCCTCAATTAAGCTATCTCTTAAACCTCTTCTCAATCTCCCTGATATCTGTAAC 1184
QY 613 CCGTAGAGTGTGTTCTCAATATTTCTGCTCCCTCTGAGATCATTAATGTCCTCAC 672
DB 1185 CCGTAGAGTGTGTTCTCAATATTTCTGCTCCCTCTGAGATCATTAATGTCCTCAC 1244
QY 673 ATGCGCGGTTTTTCTCTGACAGCTTAAAGCTACTCTCTCACTGCTCCAGGCTCTG 732
DB 1245 ATGCGCGGTTTTTCTCTGACAGCTTAAAGCTACTCTCTCACTGCTCCAGGCTCTG 1304
QY 733 GCCCCACTTACTCTCCACCCGCTCTTCTGCGCGGAGATGCTGAGGAGAGGCTATGAT 792
DB 1305 GCCCCACTTACTCTCCACCCGCTCTTCTGCGCGGAGATGCTGAGGAGAGGCTATGAT 1364
QY 793 ACTGTGTCTCTTCTGCACTGTGTGCGCGGAGAGATCATTAATGATGACCTGCTG 852
DB 1365 ACTGTGTCTCTTCTGCACTGTGTGCGCGGAGAGATCATTAATGATGACCTGCTG 1424
QY 853 CTTCATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 891
DB 1425 CTTCATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1463

```

```

RESULT 5
AB031480 1143 bp mRNA linear PRI 08-DEC-1999
LOCUS Homo sapiens SPRI mRNA, complete cds.
DEFINITION AB031480
ACCESSION AB031480.1 GI:539433
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

```

```

REFERENCE
AUTHORS Homo sapiens (human)
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (sites)
Oka, A., Tamaiya, G., Tomizawa, M., Oka, M., Katsuyama, Y., Makino, S.,
Shihina, T., Yoshitome, M., Iizuka, M., Saseo, Y., Iwashita, K.,
Kawakubo, Y., Sugai, J., Ozawa, A., Ohkido, M., Kimura, M., Bahram, S.
and Inoko, H.

```

```

TITLE Association analysis using refined microsatellite markers localizes
a susceptibility locus for psoriasis vulgaris within a 111 kb
segment telomeric to the HLA-C gene
JOURNAL Hum. Mol. Genet. 8 (12), 2165-2170 (1999)
MEDLINE 20014706
PUBMED 10545595
REFERENCE 2 (bases 1 to 1143)
AUTHORS Tamaiya, G., Tomizawa, M., Makino, S., Oka, A., Nakajima, K., Kimura, M.
and Inoko, H.
TITLE Direct Submission
JOURNAL Submitted (25-AUG-1999) Akira Oka, Tokai University School of
Medicine, Division of Molecular Life Science, Bonseidai, Isehara,
Kanagawa 259-1193, Japan (E-mail:oka246@is.icc.u-tokai.ac.jp,
Tel:81-463-93-1121(ex.2579), Fax:81-463-94-8884)
FEATURES
source
1..1143
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
/sex="male"
/cell_type="epidermal keratinocytes"
1..1143
/gene="SPRI"
316..726
/gene="SPRI"
/codon_start=1
/protein_id="BA88131.1"
/db_xref="GI:6539434"
/translation="MTLNLKLLGLIVLCLHTRGISSEBHPSPAPEDREBAGSPPLP
OGPPVDPWPVGPAPLPFEDPPTPRSPRPMDLPETGVWPEPPTDPPQPPRDPDWP
AGQPENPWPAPAEVDNRPQEBPDLPPEBYR"
ORIGIN
Query Match 87.7%; Score 781; DB 9; Length 1143;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 831; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 60 AGCCATGATCTCAATGAGAGCTCCGGGATCTGATCTTGTGCTGACACAGAGG 119
DB 312 AGCCATGATCTCAATGAGAGCTCCGGGATCTGATCTTGTGCTGACACAGAGG 371
QY 120 CATCTCAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 179
DB 372 CATCTCAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 431
QY 180 CTCCGCAACATTTGCTCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 239
DB 432 CTCCGCAACATTTGCTCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 491
QY 240 TCTCTTGAAGATCTCTGCTACCCGCTACCCGCTACCCGCTACCCGCTACCCGCTACCCGCT 239
DB 492 TCTCTTGAAGATCTCTGCTACCCGCTACCCGCTACCCGCTACCCGCTACCCGCTACCCGCT 551
QY 300 TGAAGTCTGAGCCCTCTGAACCGCTTGAACCGATCTCTCAACCTTCCGCGCTGACGA 359
DB 552 TGAAGTCTGAGCCCTCTGAACCGCTTGAACCGATCTCTCAACCTTCCGCGCTGACGA 611
QY 360 CCTTGGCCCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 419
DB 612 CCTTGGCCCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 671
QY 420 CAACCGACTCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 479
DB 672 CAACCGACTCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 731
QY 480 TCCCTCAGCGCTCTGTCTTCCAGAGCATCTCAGGAGACCCAGCCCTTCTCACCTCTGA 539
DB 732 TCCCTCAGCGCTTCTGTCTTCCAGAGCATCTCAGGAGACCCAGCCCTTCTCACCTCTGA 791
QY 540 TTCCCGGTGAATTTCTTCCCAATTAAGGCTATCTCTTAAACCTTCTCTATCTCCCTGG 599

```


Db 792 TTCCCGGTAATCTTCCCAATTTAGCTATCTCTTAAACCTCTCTCCTCCTCGG 851
Qy 600 TTTTATCTGAACCCGTAAGGTGGTGTCTCAATATTTCTGTCCTCCCTCGAGATCAT 659
Db 852 TTTTATCTGAACCCGTAAGGTGGTGTCTCAATATTTCTGTCCTCCCTCGAGATCAT 911
Qy 660 ACTTATGCTCACAATCGCCGGTTTTTCTCTGACAGCTTAAGCTTACTCTCACTCG 719
Db 912 ACTTATGCTCACAATCGCCGGTTTTTCTCTGACAGCTTAAGCTTACTCTCACTCG 971
Qy 720 CTTCCAGGCTCGGCGCCCACTTACCTCCACCGGCTTCTCTGCGCGGAGATGCTGG 779
Db 972 CTTCCAGGCTCGGCGCCCACTTACCTCCACCGGCTTCTCTGCGCGGAGATGCTGG 1031
Qy 780 GCGGGCTATGTAATCTGTTTCCCTTCTGCACTGATGCGCGGCGAGAACTATCAG 839
Db 1032 GCGGGCTATGTAATCTGTTTCCCTTCTGCACTGATGCGCGGCGAGAACTATCAG 1091
Qy 840 TAGACAGCTGCTGCTTCCATGAACGAAAAATATAATCATGTTTCTTAA 891
Db 1092 TAGACAGCTGCTGCTTCCATGAACGAAAAATATAATCATGTTTCTTAA 1143
RESULT 6
AX477396 2997 bp DNA linear PAT 12-AUG-2002
LOCUS Sequence 10 from Patent W00244375.
DEFINITION AX477396
ACCESSION AX477396
VERSION AX477396.1 GI:22216625
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Charnley, P., Moss, P. and Mceuen, M.
TITLE Compositions and methods for diagnosing or treating psoriasis
JOURNAL Patent: WO 0244375-A 10 06-JUN-2002;
Celltech R & D, Inc. (US)
FEATURES
Location/Qualifiers
1..2997
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 87.0%; Score 775; DB 6; Length 2997;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 775; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 117 AGGATCTCAGGCGAGGAGGCGCCCTCTCACCACCGGAGAGAGAGAGAGGC 176
Db 2200 AGGATCTCAGGCGAGGAGGCGCCCTCTCACCACCGGAGAGAGAGAGAGGC 2259
Qy 177 AGGCTCCCAACATTTGCTCAGGAGCCCGGAGTCCCGGAGTACCTTGGCCAGGAGACC 236
Db 2260 AGGCTCCCAACATTTGCTCAGGAGCCCGGAGTCCCGGAGTACCTTGGCCAGGAGACC 2319
Qy 237 CCCTCTTTGAAGATCTTCGCGCTTACCGGCGGAGTGTCTCTGAGAGAGACTGCTGA 296
Db 2320 CCCTCTTTGAAGATCTTCGCGCTTACCGGCGGAGTGTCTCTGAGAGAGACTGCTGA 2379
Qy 297 AACTGAGTCTGGCCCTCTGAACCGGCTTAAGAGGATCTTCTCAACTCCCGGCTGA 356
Db 2380 AACTGAGTCTGGCCCTCTGAACCGGCTTAAGAGGATCTTCTCAACTCCCGGCTGA 2439
Qy 357 CGACCTTGGCGCGGAG 416
Db 2440 CGACCTTGGCGCGGAG 2499
Qy 417 GGAACACCGAGCTTGAAG 476
Db 2500 GGAACACCGAGCTTGAAG 2559

Qy 477 GAGTCCCTCAGCGGTTCTGTTCCAGAGCATCTCAGAGCAGCAGCGGCTCTCCACCTC 536
Db 2560 GAGTCCCTCAGCGGTTCTGTTCCAGAGCATCTCAGAGCAGCAGCGGCTCTCCACCTC 2619
Qy 537 TGAATCCCGTGAATTTCTCCAAATTTAGCTATCTCTTAAACCTTCTCCTATTCCT 596
Db 2620 TGAATCCCGTGAATTTCTCCAAATTTAGCTATCTCTTAAACCTTCTCCTATTCCT 2679
Qy 597 CGGTTTTATCTGAACCCGTAAGGTGGTGTCTCAATATTTCTGTCCTCCCTCTGAGATC 656
Db 2680 CGGTTTTATCTGAACCCGTAAGGTGGTGTCTCAATATTTCTGTCCTCCCTCTGAGATC 2739
Qy 657 CATACTTATGCTCACAATCGCCGGTTTTTCTCTGACAGCTTAAGCTTACTCTCAGC 716
Db 2740 CATACTTATGCTCACAATCGCCGGTTTTTCTCTGACAGCTTAAGCTTACTCTCAGC 2799
Qy 717 TCGCTTCAGAGCTCGGCGCCCACTTACCTTCCACCGGCTTCTCTGCGCGGAGTGC 776
Db 2800 TCGCTTCAGAGCTCGGCGCCCACTTACCTTCCACCGGCTTCTCTGCGCGGAGTGC 2859
Qy 777 GGGGAGGCTATGTAATCTGTTTCCCTTCTGCACTGATGCGCGGCGAGAACTAT 836
Db 2860 GGGGAGGCTATGTAATCTGTTTCCCTTCTGCACTGATGCGCGGCGAGAACTAT 2919
Qy 837 CAGTAGACAGCTGCTGCTTCCATGAACGAAAAATATAATCATGTTTCTTAA 891
Db 2920 CAGTAGACAGCTGCTTCCATGAACGAAAAATATAATCATGTTTCTTAA 2974

RESULT 7
AX477390 3001 bp DNA linear PAT 12-AUG-2002
LOCUS Sequence 4 from Patent W00244375.
DEFINITION AX477390
ACCESSION AX477390
VERSION AX477390.1 GI:22216619
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Charnley, P., Moss, P. and Mceuen, M.
TITLE Compositions and methods for diagnosing or treating psoriasis
JOURNAL Patent: WO 0244375-A 4 06-JUN-2002;
Celltech R & D, Inc. (US)
FEATURES
Location/Qualifiers
1..3001
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 87.0%; Score 775; DB 6; Length 3001;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 775; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 117 AGGATCTCAGGCGAGGAGGCGCCCTCTCACCACCGGAGAGAGAGAGAGAGGC 176
Db 2204 AGGATCTCAGGCGAGGAGGCGCCCTCTCACCACCGGAGAGAGAGAGAGAGGC 2263
Qy 177 AGGCTCCCAACATTTGCTCAGGAGCCCGGAGTCCCGGAGTACCTTGGCCAGGAGACC 236
Db 2264 AGGCTCCCAACATTTGCTCAGGAGCCCGGAGTCCCGGAGTACCTTGGCCAGGAGACC 2323
Qy 237 CCCTCTTTGAAGATCTTCGCGCTTACCGGCGGAGTGTCTCTGAGAGAGACTGCTGA 296
Db 2324 CCCTCTTTGAAGATCTTCGCGCTTACCGGCGGAGTGTCTCTGAGAGAGACTGCTGA 2383
Qy 297 AACTGAGTCTGGCCCTCTGAACCGGCTTAAGAGGATCTTCTCAACTCCCGGCTGA 356
Db 2384 AACTGAGTCTGGCCCTCTGAACCGGCTTAAGAGGATCTTCTCAACTCCCGGCTGA 2443

QY 357 CGACCTTGGCGGCGAGAGACCCAGACCCCGAGAAAACCCCTGAGCTCTGAGGT 416
 Db 2444 CGACCTTGGCGGCGAGAGACCCAGACCCCGAGAAAACCCCTGAGCTCTGAGGT 2503
 QY 417 GGACCAACCGACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 476
 Db 2504 GGACCAACCGACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2563
 QY 477 GAGTCCCTCGAGCGGTCTGTTTCCAGAGCATCTCAGGACACCGAGCTCTCAGCTC 536
 Db 2564 GAGTCCCTCGAGCGGTCTGTTTCCAGAGCATCTCAGGACACCGAGCTCTCAGCTC 2623
 QY 537 TGATTTCCCGTGAATTTCTTCCCAATTTAGCTATCTCTTAAACCTCTTCTCAATTCCT 596
 Db 2624 TGATTTCCCGTGAATTTCTTCCCAATTTAGCTATCTCTTAAACCTCTTCTCAATTCCT 2683
 QY 597 CGGTTTATTTCTGAACCCGTAAGGTGTGTCTCAATATTTCTGTCTCTGAGATC 656
 Db 2684 CGGTTTATTTCTGAACCCGTAAGGTGTGTCTCAATATTTCTGTCTCTGAGATC 2743
 QY 657 CATACTAGTCTCAACATCCGCGGTTTCTCTGACAGCTTAACTCTCTCTAC 716
 Db 2744 CATACTAGTCTCAACATCCGCGGTTTCTCTGACAGCTTAACTCTCTCTAC 2803
 QY 717 TCGGCTCCAGGCTCTGAGCCCACTTACTCCACCCGCTCTTCTGCGCGAGTGCCT 776
 Db 2804 TCGGCTCCAGGCTCTGAGCCCACTTACTCCACCCGCTCTTCTGCGCGAGTGCCT 2863
 QY 777 GGGGCAAGGCTATGATGATGTTTCTCTTCTGCACTGTGCGCGGAGAGACTAT 836
 Db 2864 GGGGCAAGGCTATGATGATGTTTCTCTTCTGCACTGTGCGCGGAGAGACTAT 2923
 QY 837 CAGTGAACAGCTGCTGCTTCATGAAACGGAATAATTAATCTTTCTTAA 891
 Db 2924 CAGTGAACAGCTGCTGCTTCATGAAACGGAATAATTAATCTTTCTTAA 2978

RESULT 8
 LOCUS AC0004195 40878 bp DNA linear PRI 08-DEC-1998
 DEFINITION Homo sapiens clone UMG:Y24C027 from 6p21, complete sequence.
 AC0004195
 VERSION AC0004195.1 GI:3980474
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 40878)
 Jaber, M., Guillaudoux, T., Vu, Q., Kutyavin, T., Harter, H. and
 Geraghty, D.E.
 TITLE Large scale sequence analysis of the human MHC class I region
 JOURNAL Unpublished (1998)
 REMARK Fred Hutchinson Cancer Research Center
 The Clinical Research Division
 1100 Fairview Ave. N., P.O. Box 19024
 Seattle, WA 98109-1024
 Contact: Daniel E. Geraghty (geraghty@fhcrc.org)
 2 (bases 1 to 40878)
 Geraghty, D.E. and Olson, M.V.
 TITLE Direct Submission
 JOURNAL Submitted (23-FEB-1998) Human Genome Center, University of
 Washington, Box 352145, Seattle, WA 98195, USA
 3 (bases 1 to 40878)
 Geraghty, D.E. and Olson, M.V.
 TITLE Direct Submission
 JOURNAL Submitted (08-DEC-1998) Human Genome Center, University of
 Washington, Box 352145, Seattle, WA 98195, USA
 University of Washington Human Genome Center
 Box 352145 Seattle, WA 98195
 Contact: Daniel E. Geraghty (geraghty@fhcrc.org)
 On Dec 8, 1998 this sequence version replaced gi:2905865.
 COMMENT Overlapping sequences:

5' : UMG:Y14C057 (Genbank Accession: AC006047)
 3' : UMG:Y24C203

 Sequence Quality Assessment:
 This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
 Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.
 Double stranded (DS) coverage: 77.6%
 DS or two chemistry coverage: 100.0%
 Single stranded regions: 0

 Sequence Validation:
 This sequence has been validated by Multiple Complete Digest Mapping. Comparison of the experimentally derived map digest fragments with sequence-predicted fragments is given below. Small fragments below a variable cutoff (approximately 400-600bp) are not mapped and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragment groups are separated by dashed lines.

Map	BglII	HindIII	NotI
Seq	Seq	Seq	Seq
5056.53	5005.00	979.90	957.00
2289.48	2257.00	3644.92	3580.00
5302.18	5207.00	5611.48	5525.00
894.03	880.00	4618.79	4525.00
3041.57	2999.00	1532.79	1530.00
14697.70	14691.00	1726.25	1724.00
		1479.40	1473.00
		909.61	880.00
		8223.42	7996.00
		2404.83	2380.00
		7342.43	7194.00

 FEATURES
 Source
 Location/Qualifiers
 1. 40878
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6p21"
 /clone="CGM1.A194D6"
 /sub_clone="UMG:Y24C027"
 /cell_line="CGM1"
 /clone_lib="Wash U YAC Library"
 complement(4237..4519)
 /rpt_family="Alu"
 complement(4643..5052)
 /rpt_family="Alu"
 5090..5149
 /rpt_family="MIR"
 9346..9586
 /rpt_family="Alu"
 complement(9800..10094)
 /rpt_family="Alu"
 11553..11834
 repeat_region
 repeat_region
 repeat_region
 repeat_region

```

repeat_region      /rpt_family="Alu"
12152..12410
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
12650..13079
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
13401
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
15686
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
15711..15969
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
16248
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
17434..17719
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
17993..18283
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
19046..19327
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
20915..21197
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
21343..21613
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
23590..23889
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
23940..24065
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
24066..24312
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
24673..24731
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
24760..25051
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
27927..28526
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
28990..29269
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
29340..29635
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
29889..30145
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
30290..30564
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
30791..31421
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
32533..33421
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
33782..34080
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
34426..35134
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
35292..35444
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
37575..37780
/rpt_family="Alu"
repeat_region      /rpt_family="Alu"
40636..40717
/rpt_family="Alu"

ORIGIN
Query Match      87.0%; Score 775; DB 9; Length 40878;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 775; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      117 AGGATCTCAGGCGAGGCGACCCCTCTCACCACCGCAGAGAGACCGAGAGAGC 176
      |||
DB      27087 AGGCATCTCAGGCGAGGCGACCCCTCTCACCACCGCAGAGAGACCGAGAGAGC 27146

QY      177 AGGCTCCCAACATTCGCTCAGGCGCGCCGAGTACCGCTGCGCAGAGAGAGC 236
      |||
DB      27147 AGGCTCCCAACATTCGCTCAGGCGCGCCGAGTACCGCTGCGCAGAGAGAGC 27206

QY      237 CCCTCTCTTGAAGATCTCCGCGCTACCGCGCCGAGTCTGCTGAGAGAGACTGCGCTGA 296
      |||

```

```

DB      27207 CCCTCTCTTGAAGATCTCCGCGCTACCGCGCCGAGTCTGCTGAGAGAGACTGCGCTGA 27266
QY      297 AACTGAGTCTGAGCCCTTGAACCGCTTGAAGAGATCCCTCAACCTCCCGGCTGA 356
      |||
DB      27267 AACTGAGTCTGAGCCCTTGAACCGCTTGAAGAGATCCCTCAACCTCCCGGCTGA 27326
QY      357 CGACCCCTGAGCGGAGAGACCCGAGCCCGCAGAAAACCTGAGCTCTGCTCCCTGAGGT 416
      |||
DB      27327 CGACCCCTGAGCGGAGAGACCCGAGCCCGCAGAAAACCTGAGCTCTGCTCCCTGAGGT 27386
QY      417 GGAACAACGACCTCAGAGAGAGGCGAGACCTGACCAACCCCGGAGAGATACATATATG 476
      |||
DB      27387 GGAACAACGACCTCAGAGAGAGGCGAGACCTGACCAACCCCGGAGAGATACATATATG 27446
QY      477 GAGTCCCTCAGCGCTTCTGTTCCGAGCATCTCCAGGACCCGAGCCCTCTCAGCTTC 536
      |||
DB      27447 GAGTCCCTCAGCGCTTCTGTTCCGAGCATCTCCAGGACCCGAGCCCTCTCAGCTTC 27506
QY      537 TGAATCCCGTGAATCTTCCCAATTTAGGCTATCTCTTAAACCTTCTGATTCCT 596
      |||
DB      27507 TGAATCCCGTGAATCTTCCCAATTTAGGCTATCTCTTAAACCTTCTGATTCCT 27566
QY      597 CGGTTTATTTCTGAACCCGTAAGGTGTCTCAATATTTCTGTCCTCTGAGATC 656
      |||
DB      27567 CGGTTTATTTCTGAACCCGTAAGGTGTCTCAATATTTCTGTCCTCTGAGATC 27626
QY      657 CATACTAGTCTCAATGCGCCGCTTTTCTCTGACAGCCTTAAGCTACTCTCTACC 716
      |||
DB      27627 CATACTAGTCTCAATGCGCCGCTTTTCTCTGACAGCCTTAAGCTACTCTCTACC 27686
QY      717 TCGCCTCAGAGCTCGGCGCCACCTACCTCCACCGGCTTCTCTGCGCGGAGATGCT 776
      |||
DB      27687 TCGCCTCAGAGCTCGGCGCCACCTACCTCCACCGGCTTCTCTGCGCGGAGATGCT 27746
QY      777 GGGGCAAGGCTATAGTACTGTGTCTTCTGACACCTGTGTGCGCGGAGAACTAT 836
      |||
DB      27747 GGGGCAAGGCTATAGTACTGTGTCTTCTGACACCTGTGTGCGCGGAGAACTAT 27806
QY      837 CAGTAGACACTGTGTTTCCATGAAACGAAATTAATATGATTTTCTTAA 891
      |||
DB      27807 CAGTAGACACTGTGTTTCCATGAAACGAAATTAATATGATTTTCTTAA 27861

RESULT 9
AL773544/c      113388 bp      DNA      linear      PRI 21-OCT-2003
LOCUS
DEFINITION
Human DNA sequence from clone DaQB-18511 on chromosome 6, complete
sequence.
ACCESSION
AL773544
VERSION
AL773544.5 GI:37805611
KEYWORDS
HTG.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 113388)
AUTHORS
Almeida,J.
TITL
Direct Submission
JOURNAL
Submitted (21-OCT-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Oct 21, 2003 this sequence version replaced gi:22759515.

COMMENT
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
-----

```

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone conigs constructed by the MHC HaploTYPE Consortium and collaborators. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr6/MHC>

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

DAOB-18511 is from a DNA-arts QBL human bac library VECTOR: pBelobAC11.

FEATURES
source

1. 113388
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/clone="DAOB-18511"
/clone_lib="DNA-arts-BAC-1-QBL.1"

ORIGIN

Query Match 81.7%; Score 728; DB 9; Length 113388;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

117 AGGCATCTGAGGCGAGGCGGACCCCTCTCAACCCGAGAGAGAGAGAGAGGCG 176
60144 AGGCATCTGAGGCGAGGCGGACCCCTCTCAACCCGAGAGAGAGAGAGAGGCG 60085
177 AGGCTCCCAACATTTGGCTTCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 236
60084 AGGCTCCCAACATTTGGCTTCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60025
237 CCTCTCTTTGAAGATCTCGGCTTACCCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 296
60024 CCTCTCTTTGAAGATCTCGGCTTACCCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 59965
297 AACTGAGTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 356
59964 AACTGAGTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 59905
357 CGACCTTGGCGGCGAGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 416
59904 CGACCTTGGCGGCGAGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 59845
417 GGAACAACCGACTCAG 476
59844 GGAACAACCGACTCAG 59785
477 GAGTCCCTCAGCGGCTTCTGTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 536
59784 GAGTCCCTCAGCGGCTTCTGTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 59725
537 TGAATCCCGGTAATTTCTCCCAATTTAGCTTAACTTCTTAACTTCTTAACTTCT 596
59724 TGAATCCCGGTAATTTCTCCCAATTTAGCTTAACTTCTTAACTTCTTAACTTCT 59665
597 CGGTTTATTTCTGAACCCGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 656
59664 CGGTTTATTTCTGAACCCGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 59605
657 CATACTAGTCTCAATCGCGGCTTTTCTCTGAGAGAGAGAGAGAGAGAGAGAGAG 716
59604 CATACTAGTCTCAATCGCGGCTTTTCTCTGAGAGAGAGAGAGAGAGAGAGAGAG 59545

QY 717 TCGGCTTCAGAGCCTTCGAGCCCGGACCTTACCTCCACCGGCTTTCTGCGCGGAGATGCT 776
Db 59544 TCGGCTTCAGAGCCTTCGAGCCCGGACCTTACCTCCACCGGCTTTCTGCGCGGAGATGCT 59485
QY 777 GGGGCAAGGCTATGATGATCTGTGTTCCCTTCTGACACCTGATGAGCGGCGGAGAACTAT 836
Db 59484 GGGGCAAGGCTATGATGATCTGTGTTCCCTTCTGACACCTGATGAGCGGCGGAGAACTAT 59425
QY 837 CAGTAGAC 844
Db 59424 CAGTAGAC 59417
RESULT 10
BD095297
LOCUS The method of testing for psoriasis vulgaris.
ACCESSION BD095297
VERSION BD095297.1 GI:22640885
KEYWORDS WO 0142458-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Inoko, H. and Tamiya, G.
TITLES The method of testing for psoriasis vulgaris
JOURNAL Patent: WO 0142458-A 2 14-JUN-2001;
HIDETOSHI INOKO, GEN TAMIIYA
OS Homo sapiens (human)
PN WO 0142458-A/2
PD 14-JUN-2001
PR 06-DEC-2000 WO 2000JP008624
PR 06-DEC-1999 JP 99P 346867
PI HIDETOSHI INOKO, GEN TAMIIYA
PC C12N15/12, C12Q1/68
CC The method of testing for psoriasis vulgaris
FT Key Location/Qualifiers
FT exon (1) . (420)
FT exon (1282) . (1405)
FT exon (1602) . (1702)
FT exon (1602) . (1631)
FT exon (2352) . (2364)
FT exon (6287) . (6509)
FT exon (10417) . (10493)
FT exon (14244) . (14407)
FT exon (14244) . (14344)
FT exon (25190) . (25235).
FEATURES
source
1. 25235
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 81.3%; Score 724; DB 6; Length 25235;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 774; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 117 AGGCATCTGAGGCGAGGCGGACCCCTCTCAACCCGAGAGAGAGAGAGAGGCG 176
Db 1753 AGGCATCTGAGGCGAGGCGGACCCCTCTCAACCCGAGAGAGAGAGAGAGGCG 1812
QY 177 AGGCTCCCAACATTTGGCTTCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 236
Db 1813 AGGCTCCCAACATTTGGCTTCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 18172
QY 237 CCTCTCTTTGAAGATCTCTCGGCTTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 296
Db 1873 CCTCTCTTTGAAGATCTCTCGGCTTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1932
QY 297 AACTGAGTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 356

[illegible]

HPELFASVLPMAPEBAARLQOPPLPPSGIHLASBRLAFTLLYSSPSHPGLSS
 LI"
 29079. .29448
 /gene="SEKI"
 /number=1
 29748. .30167
 /number=6

Query Match 81.3%; Score 724; DB 9; Length 30911;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 774; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 117 AGGCATCTCAGCAGCAGGAGGAGCCCTCTCACCACCCGAGAGAGCAGAGAGGC 176
 28415 AGGCATCTCAGCAGCAGGAGGAGCCCTCTCACCACCCGAGAGAGCAGAGAGGC 28356
 Qy 177 AGGCTCCCAACATTGCTCTCAGGAGGAGCCCTCTCACCACCCGAGAGAGC 236
 28355 AGGCTCCCAACATTGCTCTCAGGAGGAGCCCTCTCACCACCCGAGAGAGC 28296
 Db 237 CCCTCTCTTGAAGATCCTCGGCTTACCGGCTTACCGGCTTACCGGCTTACCGGCTT 296
 28295 CCCTCTCTTGAAGATCCTCGGCTTACCGGCTTACCGGCTTACCGGCTTACCGGCTT 28236
 Qy 297 AACTGAGTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 356
 28235 AACTGAGTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 28176
 Db 357 CGAGCCCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 416
 28175 CGAGCCCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 28116
 Qy 417 GGAACAACGAGCCTCAGAGAGAGCAGAGCCTGAGCCACCCGAGAGAGTACAGATATG 476
 28115 GGAACAACGAGCCTCAGAGAGAGCAGAGCCTGAGCCACCCGAGAGAGTACAGATATG 28056
 Db 477 GAGTCCCTCTCAGCCCTCTGAGCCCTCTCAGCCCTCTCAGCCCTCTCAGCCCTCT 536
 28055 GAGTCCCTCTCAGCCCTCTGAGCCCTCTCAGCCCTCTCAGCCCTCTCAGCCCTCT 27996
 Qy 537 TGATTCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 596
 27995 TGATTCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 27936
 Db 597 CGGTTTATCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 656
 27935 CGGTTTATCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 27876
 Qy 657 CATACTTATCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 716
 27875 CATACTTATCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 27816
 Db 717 TCGCCTCTCAGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 776
 27815 TCGCCTCTCAGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 27756
 Qy 777 GGGGACAGGCTATGATCTGTGTTCCCTTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 836
 27755 GGGGACAGGCTATGATCTGTGTTCCCTTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 27696
 Db 837 CAGTGAAGCAGCTCTGTTTCCATGAAACGAAATTAATATCATGTTTCTTAA 891
 27695 CAGTGAAGCAGCTCTGTTTCCATGAAACGAAATTAATATCATGTTTCTTAA 27641

RESULT 12
 AB023060
 LOCUS Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region,
 DEFINITION AB023060
 ACCESSION AB023060
 VERSION AB023060.1 GI:5672629

KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1 (sites)

AUTHORS
 Shihina,T., Tamura,G., Oka,A., Takishima,N., Yamagata,T.,
 Kikawa,E., Iwata,K., Tomizawa,M., Okunaka,N., Kuwano,Y.,
 Watanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,
 Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,
 Bahram,S., and Inoko,H.
 Molecular dynamics of MHC genesis unraveled by sequence analysis of
 the 1,796,938-bp HLA class I region
 Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)

TITLE

JOURNAL
 MEDLINE
 PUBMED

10557312
 2 (bases 1 to 39196)

Shihina,T. and Takishima,N.
 Direct Submission

JOURNAL

Submitted (29-JAN-1999) Takashi Shihina, Tokai University School of
 Medicine, Department of Molecular Life Science 2, Bohseidai,
 Isehara, Kanagawa 259-1193, Japan
 E-mail: tshihina@is.tokai.ac.jp, Tel: 81-463-93-1121,
 Fax: 81-463-94-8884

FEATURES

source

1. .39196
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6p21.3"
 /clone="TYIC2"
 /cell_line="BOLETH"
 /tissue_type="B cell line"

ORIGIN

Query Match 81.3%; Score 724; DB 9; Length 39196;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 774; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 117 AGGCATCTCAGCAGGAGGAGCCCTCTCACCACCCGAGAGAGCAGAGAGGC 176
 Db 10633 AGGCATCTCAGCAGGAGGAGCCCTCTCACCACCCGAGAGAGCAGAGAGGC 10692
 Qy 177 AGGCTCCCAACATTGCTCTCAGGAGGAGCCCTCTCACCACCCGAGAGAGC 236
 10693 AGGCTCCCAACATTGCTCTCAGGAGGAGCCCTCTCACCACCCGAGAGAGC 10732
 Db 10693 AGGCTCCCAACATTGCTCTCAGGAGGAGCCCTCTCACCACCCGAGAGAGC 10732
 Qy 237 CCCTCTCTTGAAGATCTCGGCTTACCGGCTTACCGGCTTACCGGCTTACCGGCTT 296
 10753 CCCTCTCTTGAAGATCTCGGCTTACCGGCTTACCGGCTTACCGGCTTACCGGCTT 10812
 Db 297 AACTGAGTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 356
 10813 AACTGAGTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 10872
 Qy 357 CGACCTTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 416
 10873 CGACCTTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 10932
 Db 417 GGAACAACGAGCCTCAGAGAGAGCAGAGCCTGAGCCACCCGAGAGAGTACAGATATG 476
 10933 GGAACAACGAGCCTCAGAGAGAGCAGAGCCTGAGCCACCCGAGAGAGTACAGATATG 10992
 Qy 477 GAGTCCCTCTCAGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 536
 10993 GAGTCCCTCTCAGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 11052
 Db 537 TGATTCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 596
 11053 TGATTCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 11112
 Qy 597 CGGTTTATCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCTGAGCCCTCT 656

```

Db      11113 CGGTTTATTCTGAACCGTAGGAGTGCTCAATATTTCTGTCCCTCTGAGATC 11172
Qy      657 CATACTAGTCCACATTCGCGCGTTTCTCTGACAGCTAAGCTATCTCCACC 716
Db      11173 CATCTTAGTCTCAATCGCGCTTTTCTCTGACAGCTAAGCTATCTCTACC 11232
Qy      717 TCGGCTCAGGCTCGGCGCCACCTACCTCCACCGGCTCTCTGCGCGGAGTGCCT 776
Db      11233 TCGGCTCAGGCTCGGCGCCACCTACCTCCACCGGCTCTCTGCGCGGAGTGCCT 11292
Qy      777 GGGGCAAGGCTAAGTACTGTCTCTGCGACCTGTGCGCGGCGGAGAACTAT 836
Db      11293 GGGGCAAGGCTAAGTACTGTCTCTGCGACCTGTGCGCGGCGGAGAACTAT 11352
Qy      837 CAGTAGACAGCTGCTCTCCATGAAACGAAAAATATAATCATGTTTCTTAA 891
Db      11353 CAGTAGACAGCTGCTCTCCATGAAACGAAAAATATAATCATGTTTCTTAA 11407

```

RESULT 13

```

AX522117 55050 bp DNA linear PAT 24-OCT-2002
LOCUS      Sequence 4 from Patent WO02064831.
DEFINITION AX522117
ACCESSION  AX522117
VERSION     AX522117.1 GI:24411002
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Eukaryota; Mammalia; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1
AUTHORS     Lench, N.J., Allen, M.J. and Nicholas, R.K.
TITLES      Test and model for inflammatory disease
JOURNAL     Patent: WO 02064831-A 4 22-AUG-2002;
            Oxagen Limited (GB)
FEATURES
            Location/Qualifiers
            source          1..55050
                           /organism="Homo sapiens"
                           /mol_type="unassigned DNA"
                           /db_xref="taxon:9606"

```

ORIGIN

```

Query Match      81.3%; Score 724; DB 6; Length 55050;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 774; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      117 AGGCATCTCAGGCGAGGCGCACCCCTCTCAACCCGCAAGAGACCGAGAGAGC 176
Db      27098 AGGCATCTCAGGCGAGGCGCACCCCTCTCAACCCGCAAGAGACCGAGAGAGC 27157
Qy      177 AGGCTCCCAACATTCCTTCAAGGCGCGCCCAAGTCCCGGTGACCTTGGCCAGGGCAAC 236
Db      27158 AGGCTCCCAACATTCCTTCAAGGCGCGCCCAAGTCCCGGTGACCTTGGCCAGGGCAAC 27217
Qy      237 CCGCTCTTGAAGATCTCGGCTACCGCGCCAGTCCCTCGAGAGACCTGCGCTGA 296
Db      27218 CCGCTCTTGAAGATCTCGGCTACCGCGCCAGTCCCTCGAGAGACCTGCGCTGA 27277
Qy      297 AACTGAGTGTGGCCCTTGAACCGCTAGAACGATCTCTCAACCTCCCGGCTGA 356
Db      27278 AACTGAGTGTGGCCCTTGAACCGCTAGAACGATCTCTCAACCTCCCGGCTGA 27337
Qy      357 CGACCTTGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 416
Db      27338 CGACCTTGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 27397
Qy      417 GGAACAACGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATG 476
Db      27398 GGAACAACGAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATG 27457
Qy      477 GAGTCCCTCAGGCGGTCTGTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 536

```

```

Db      27458 GAGTCCCTCAGGCGGTCTGTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 27517
Qy      537 TGAATCCCGGAGATTCCTCCAAATTAAGCTATCTCTTAACCTCTCTCTCAATCCCT 596
Db      27518 TGAATCCCGGAGATTCCTCCAAATTAAGCTATCTCTTAACCTCTCTCTCAATCCCT 27577
Qy      597 CGGTTTATTCTGAACCGTAGGAGTGCTTCAATATTTCTGTCCCTCTGAGATC 656
Db      27578 CGGTTTATTCTGAACCGTAGGAGTGCTTCAATATTTCTGTCCCTCTGAGATC 27637
Qy      657 CATCTTAGTCTCAATTCGCGGTTTCTCTGACAGCTAAGCTATCTCTACC 716
Db      27638 CATCTTAGTCTCAATTCGCGGTTTCTCTGACAGCTAAGCTATCTCTACC 27697
Qy      717 TCGGCTCAGGCTCGGCGCCACCTACCTCCACCGGCTCTCTGCGCGGAGTGCCT 776
Db      27698 TCGGCTCAGGCTCGGCGCCACCTACCTCCACCGGCTCTCTGCGCGGAGTGCCT 27757
Qy      777 GGGGCAAGGCTAAGTACTGTCTCTGCGACCTGTGCGCGGCGGAGAACTAT 836
Db      27758 GGGGCAAGGCTAAGTACTGTCTCTGCGACCTGTGCGCGGCGGAGAACTAT 27817
Qy      837 CAGTAGACAGCTGCTCTCCATGAAACGAAAAATATAATCATGTTTCTTAA 891
Db      27818 CAGTAGACAGCTGCTCTCCATGAAACGAAAAATATAATCATGTTTCTTAA 27872

```

RESULT 14

```

AL662867/c 70288 bp DNA linear PRI 24-APR-2002
LOCUS      Human DNA sequence from clone Xxbac-34D1 on chromosome 6, complete
DEFINITION AL662867
ACCESSION  AL662867
VERSION     AL662867.5 GI:20068664
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Eukaryota; Mammalia; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1
AUTHORS     Sycamore, N.
TITLES      Direct Submission
JOURNAL     Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
            On Apr 7, 2002 this sequence version replaced gi:19309560.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em: EMBL; SW:
            SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP
            database can be found at
            http://www.sanger.ac.uk/projects/C_elegans/wormpep Xxbac-34D1 is
            from a CHORI-502 human bac - COX cell line library VECTOR:
            pPARBAC2.1

```

COMMENT

```

This sequence was generated from part of bacterial clone configs
constructed by the MHC Haplotype Consortium and collaborators.
Further information can be found at
http://www.sanger.ac.uk/HGP/Chre/MHC.
Location/Qualifiers
            1..70288
            /organism="Homo sapiens"
FEATURES
            source

```

ORIGIN

```

/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/clone="XXbac-34D1"
/clone_lib="CHORI-502"

```

Query Match 81.3%; Score 724; DB 9; Length 70288;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 774; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 117 AGGATCTCAGGCGAGGCGGCGCCCTCTCACCCGCGAGAGACCGAGAGGCGC 176
DB 67724 AGGATCTCAGGCGAGGCGGCGCCCTCTCACCCGCGAGAGACCGAGAGGCGC 67665
QY 177 AGGCTCCCAACATTTGCTGAGGAGCGCGGCGAGTCCCGGAGACCTTGGCGAGGCGAC 236
DB 67664 AGGCTCCCAACATTTGCTGAGGAGCGCGGCGAGTCCCGGAGACCTTGGCGAGGCGAC 67605
QY 237 CCTCTCTTTGAGAGATCTCTCGCTACCGCGCGCGAGTCTCTGAGAGACCTGCTGA 236
DB 67604 CCTCTCTTTGAGAGATCTCTCGCTACCGCGCGCGAGTCTCTGAGAGACCTGCTGA 67545
QY 297 AACTGAGTCTGGCGCCCTGTAACCTGCTTAAGAGAGATCTCTGACCTCCCGGCTGA 356
DB 67544 AACTGAGTCTGGCGCCCTGTAACCTGCTTAAGAGAGATCTCTGACCTCCCGGCTGA 67485
QY 357 CGACCTCTGGCGCGGAGAGACCGCGCGCGAGAAACCTTGGCGCTCTGCGCTGAGGT 416
DB 67484 CGACCTCTGGCGCGGAGAGACCGCGCGCGAGAAACCTTGGCGCTCTGCGCTGAGGT 67425
QY 417 GAGCAACCGACCTCAGAGAGAGCGACAGCTAGACCCGCGGAGAGATACAGATATG 476
DB 67424 GAGCAACCGACCTCAGAGAGAGCGACAGCTAGACCCGCGGAGAGATACAGATATG 67365
QY 477 GAGTCCCTCTCAGCGCTTCTGTTCCAGAGCATCTCAGAGCACCGCGCTCTCCACCTTC 536
DB 67364 GAGTCCCTCTCAGCGCTTCTGTTCCAGAGCATCTCAGAGCACCGCGCTCTCCACCTTC 67305
QY 537 TGAATCCCGGAGATCTCTCCCAATTTAGCCATATCTCTTAAACCTTCTCTCATTTCCCT 596
DB 67304 TGAATCCCGGAGATCTCTCCCAATTTAGCCATATCTCTTAAACCTTCTCTCATTTCCCT 67245
QY 597 CGGTTTATTTCTGAAACCGGTAAGGTGTTCTCAATATTTCTCTGACGCTCTGAGATC 656
DB 67244 CGGTTTATTTCTGAAACCGGTAAGGTGTTCTCAATATTTCTCTGACGCTCTGAGATC 67185
QY 657 CATRATTAGTCTCAACATGCGCGGTTTTTCTCTCTGACAGCTTAAGCTTACTCTCTACC 716
DB 67184 CATRATTAGTCTCAACATGCGCGGTTTTTCTCTCTGACAGCTTAAGCTTACTCTCTACC 67125
QY 717 TCGGCTCCAGAGCGCTCGGCGCGACACTTACCTCCACCGGCTTCTGCGCGGAGATGCT 776
DB 67124 TCGGCTCCAGAGCGCTCGGCGCGACACTTACCTCCACCGGCTTCTGCGCGGAGATGCT 67065
QY 777 GGGGCAAGGGCTATGTAAGTGTCTCTCTGACAGCTTGGTGGCGCGGAGAACTAT 836
DB 67064 GGGGCAAGGGCTATGTAAGTGTCTCTCTGACAGCTTGGTGGCGCGGAGAACTAT 67005
QY 837 CAGTAGACAGCTGTGTTCCATGAAACGAAATATAATCATGTTTCTTAA 891
DB 67004 CAGTAGACAGCTGTGTTCCATGAAACGAAATATAATCATGTTTCTTAA 66950

```

RESULT 15
 AP000510
 LOCUS Homo sapiens genomic DNA, chromosome 6p21.3, HLA Class I region, section 9/20.
 ACCESSION AP000510 BA000025
 VERSION AP000510.2 GI:7380878
 KEYWORDS
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1
 Shima, S., Tamura, G., Oka, A. and Inoko, H.
 Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region
 Published Only in Database (1999)
 2 (bases 1 to 99999)
 Hirakawa, M., Yamaguchi, H., Imai, K. and Shimada, J.
 Direct Submission
 Submitted (21-SEP-1999) Miki Hirakawa, Japan Science and Technology Corporation (JST), Advanced Databases Department; 5-3, Yodancho, Chiyoda-ku, Tokyo 102-0081, Japan (E-mail: mika@okyo.jst.go.jp, URL: http://www-alis.tokyo.jst.go.jp/, Tel: 81-3-5214-8491, Fax: 81-3-5214-8470)
 On Mar 31, 2000 this sequence version replaced gi:5926697.
 This sequence is conducted by Tokai University as a JST sequencing Team.

COMMENT
 Principal Investigator: Hidetoshi Inoko Ph.D
 Phone: +81-463-93-1121, Fax: +81-463-94-8884,
 The sequence is submitted by Human Genome Sequencing in ALIS project of JST
 Japan Science and Technology Corporation (JST)
 5-3, Yodancho, Chiyoda-ku, Tokyo, 102-0081 Japan
 For further information about this sequences, please visit our
 sequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/top.
 html) or send email to webmaster@www-alis.tokyo.jst.go.jp
 Sequence updated (28-Mar-2000).

FEATURES

Source

```

1..99999
  /organism="Homo sapiens"
  /mol_type="genomic DNA"
  /db_xref="taxon:9606"
  /chromosome="6"
  /map="6p21.3"
  2016..2435
    /gene="SEBK1"
    /number=6
  complement(join(2144..2435,3297..3319))
    /gene="SEBK1"
    complement(join(2144..2435,3297..3319))
    /gene="SEBK1"
    /codon_start=1
    /protein_id="BAB63314.1"
    /db_xref="GI:15277221"
    HPELFASVLPMAPEEAARLQOPPLPPSGIHLASRTLAPTLTYSSPPSHSPFGLLS
    LI"
    join(2735..3104,3770..4542)
      /gene="SPR1"
      2735..3104
        /gene="SPR1"
        /number=1
        join(3050..3104,3770..4125)
          /gene="SPR1"
          /codon_start=1
          /protein_id="BAB63315.1"
          /db_xref="GI:15277222"
          OGPYPVGDMPGAPLPEFPPPTPSRPPWDLPEITGVMPPEPPPTDPPQPPRPDPFWP
          AGROPENPWPAPAEVDNRPOREPDLPREKRY"
          join(3297..3420,3617..3646)
            /gene="SEBK1"
            3297..3420
              /gene="SEBK1"
              /number=5
              3617..3646
                /gene="SEBK1"
                /number=4
                3770..4542
                  /gene="SPR1"

```


Gene /number=2
12432. .16422
/gene="SBEK1"
exon 12432. .12508
/gene="SBEK1"
/number=3
exon 16259. .16422
/gene="SBEK1"
/number=2
gene 21667. .27003
/gene="S"
exon 21667. .21765
/gene="S"
/number=1
cds join(21729. .21765,24570. .26074)
/gene="S"
/codon_start=1
/protein_id="BAB63316.1"
/db_xref="GI:152771223"
/translation="MALLLAGLIPGLIARSICTFSDPCKDPIRITISPNDCILTGKGA
DSGGSYSGSSSGSSISIPARSGCGSGSGSSIAQGGAGSPFKPQTVSGVSYVA
SSGCGSLQCAAGSGLGSSSHSGSGSGSGSSSHSSSSSFPSSSSFPVNGGSMAL
PINDSYRIILNPQPOGSSSSSOTSGVSSSQSVSNORPCSDIIPSPCGGPITVS
HSGVPIPSHSSVSGORPVVVYVDHGGGAGVGVGPCCNAGLPGKRCPIITVDKSS
KCGVGVSSSSSYLIPGWTYKCKITGVYKPTKMPKSGPVDSPAGAPGPIETGKSS
PESNLTIPQSSAASALIAFQPVGTGVALCGGAGTSGKGPSPSSSRVPSSSSISSSSS
GSPVHPDGSQPCSPPTGTSFSSSSSSSGKTIILQPCGSKSSSGHPCMVSVSLIL
LTGGPDGSHPDPSAGAKPFGSSSAGKIPCRSIRDIILAVKPLGQIADPVFIPQGBE
LIDSE"

exon 24570. .27003
/gene="S"
/number=2
STS 26711. .26940
/gene="S"
/note="R11634; The location is between each flanking site
of PCR primers."
gene 27205. .27250
/db_xref="CDB:4572035"
/gene="SBEK1"
exon 27205. .27250
/gene="SBEK1"
/number=1

	Query Match	Similarity	81.3%;	Score 724;	DB 9;	Length 99999;
	Best Local	Similarity	99.9%;	Pred. No. 0;		
	Matches	774;	Conservative	0;	Mismatches	1;
					Indels	0;
					Gaps	0;
QY	117	AGGATCTCAGGACGAGGGCCACCCCTCTCACCACCCCGCAGAGACCGAGAGAGGC	176			
Db	3768	AGGATCTCAGGACGAGGGCCACCCCTCTCACCACCCCGCAGAGACCGAGAGAGGC	3827			
QY	177	AGGCTCCCCCAACTTGGCTCAGGGCCCCCAAGTCCCCGGTGAACCTTGGCCAGGGGCAAC	236			
Db	3828	AGGCTCCCCCAACTTGGCTCAGGGCCCCCAAGTCCCCGGTGAACCTTGGCCAGGGGCAAC	3887			
QY	237	CCCTCTCTTTGAAGATCCTCGGCTACCCGGCCCCAGTGATGCTCGTGAAGAGACTTGCTGA	296			
Db	3888	CCCTCTCTTTGAAGATCCTCGGCTACCCGGCCCCAGTGATGCTCGTGAAGAGACTTGCTGA	3947			
QY	297	AACGTGAGTCTGGCCCCCTGAAACCGGCTAGAACGGATCTCTCAACTCCCGGCTGA	356			
Db	3948	AACGTGAGTCTGGCCCCCTGAAACCGGCTAGAACGGATCTCTCAACTCCCGGCTGA	4007			
QY	357	CGACCCCTTGGCGCGGACGAGACCCCAAGCCCCCGAAGAAACCCCTGGGCTCCTGGCCCTGAGGT	416			
Db	4008	CGACCCCTTGGCGCGGACGAGACCCCAAGCCCCCGAAGAAACCCCTGGGCTCCTGGCCCTGAGGT	4067			
QY	417	GGACAACCGAAGCTCAGAGAGACGACCTAGACCAACCCGGGAAAGTACAGTATG	476			
Db	4068	GGACAACCGAAGCTCAGAGAGAGACGACCTAGACCAACCCGGGAAAGTACAGTATG	4127			
QY	477	GAGTCCCTCAGCCGTTCTGTTCACGAGCACTCCAGGACCCAGCCCTCTCAACCTTC	536			

Db	4128	GAGTCCCCCTAGCCGTTCTGTCTCCCAAGGCACTCTCAAGGACCCAGGCCCTCTCACCCCTC	4187
QY	537	TGATTTCCCCGCTGAATTTCTTCCCAATTAGCCCTATCTCCTTAACCTCTTCTCTCATTTCCCT	596
Db	4188	TGATTTCCCCGCTGAATTTCTTCCCAATTAGCCCTATCTCCTTAACCTCTTCTCTCATTTCCCT	4247
QY	597	CGGTTTATTTCTGAACCCGTAAGGTGGTGTCTTCATATTTCTCTGTCCCTCCTGAGATC	656
Db	4248	CGGTTTATTTCTGAACCCGTAAGGTGGTGTCTTCATATTTCTCTGTCCCTCCTGAGATC	4307
QY	657	CATCTTAGTCTCTACACATCGCCGCTTTTTTCTCTGACAGCTTAAGCTTACTCTCCAC	716
Db	4308	CATCTTAGTCTCTACACATCGCCGCTTTTTTCTCTGACAGCTTAAGCTTACTCTCCAC	4367
QY	717	TTCGCTCCAGGCGCTCGGCGCCCACTACTCCCAACCGGCTTTCCTGCGCGCGGATGGCT	776
Db	4368	TTCGCTCCAGGCGCTCGGCGCCCACTACTCCCAACCGGCTTTCCTGCGCGCGGATGGCT	4427
QY	777	GGGGCAGGGGCTATGGTACTGTGTTCCCTTCGACCACTGGGTGGCGCGGCGAGAACTAT	836
Db	4428	GGGGCAGGGGCTATGGTACTGTGTTCCCTTCGACCACTGGGTGGCGCGGCGAGAACTAT	4487
QY	837	CAGTAGACAGCTGCTGCTTCATGATAACGAAAAATATTAATCATGTTTTCTTAA	891
Db	4488	CAGTAGACAGCTGCTGCTTCATGATAACGAAAAATATTAATCATGTTTTCTTAA	4542

Search completed: January 11, 2005, 10:41:26
Job time : 4031 secs

THIS PAGE BLANK (USPTO)

XX WPI; 2002-508513/54.
 DR P-PSDB; AAU79579.
 XX
 PT Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation
 PT and differentiation, and polynucleotides encoding the polypeptide, useful
 PT for diagnosing or predicting susceptibility to psoriasis in individual.
 XX
 PS Claim 8; Page 80-81, 95pp; English.

CC The invention discloses isolated candidate coding sequence-1 (CAN-1),
 CC SEK-1 (not defined) and STG (not defined) polypeptides, and the
 CC polynucleotides encoding them. All three genes were identified due to
 CC their proximity to the human leukocyte antigen C (HLA C) locus on
 CC chromosome 6. The HLA CW6 allele is associated with psoriasis and as the
 CC three genes are expressed in normal skin and/or keratinocyte tissue, they
 CC may also have a role in psoriasis. Psoriasis is a chronic inflammatory
 CC dermatosis that is characterised by hyperproliferation of epidermal
 CC cells. Possible treatments against psoriasis involve the inhibition of
 CC movement of cells into the epidermis, or the inhibition of
 CC hyperproliferation or abnormal differentiation of keratinocytes, by the
 CC inhibition of the CAN-1, STG or SEK-1 polypeptides binding to their
 CC binding partners. The polypeptides are useful for diagnosing or
 CC predicting the susceptibility to psoriasis in an individual, for
 CC ameliorating the symptoms and/or progression of psoriasis and for
 CC identifying agents useful for treating psoriasis or modulating the
 CC activity of the polypeptide. The polypeptides are also useful for
 CC enhancing the level of CAN-1, STG or SEK-1 biological activity in a cell
 CC or tissue. The nucleic acid molecules are useful as hybridisation probes
 CC in diagnostic procedures (such as diagnosing the presence of psoriasis or
 CC the propensity to develop psoriasis) and for suppressing the expression
 CC of CAN-1 or STG gene (e.g. antisense inhibition, gene therapy).
 CC Antibodies, raised against the polypeptides, are useful for decreasing
 CC the level of CAN-1, STG or SEK-1 biological activity in a cell. The
 CC sequence presented is the human candidate coding sequence-1 (CAN-1) cDNA
 XX
 XX Sequence 891 BP, 169 A; 339 C; 196 G; 187 T; 0 U; 0 Other;

Query Match 100.0%; Score 891; DB 6; Length 891;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTGGGGTTCACGACCCAGACTGACCCAGCTTTGGGGGCACTACATA 60
 Db 1 CCTCTGGGGTTCACGACCCAGACTGACCCAGCTTTGGGGGCACTACATA 60
 QY 61 GCATATATCTCTCAATGGAAGCTCTGGGATCTGTCTTGGCTGCACACAGAGC 120
 Db 61 GCATATATCTCTCAATGGAAGCTCTGGGATCTGTCTTGGCTGCACACAGAGC 120
 QY 121 ATCTCAGGACGAGGAGGACCCCTCTCAACCCAGCAGAGAGCAGAGGAGG 180
 Db 121 ATCTCAGGACGAGGAGGACCCCTCTCAACCCAGCAGAGAGCAGAGGAGG 180
 QY 181 TCCCAACATTTGCTCAGGAGCCCGGAGTCCCGGTGACCTTTGGCAGGGGCA 240
 Db 181 TCCCAACATTTGCTCAGGAGCCCGGAGTCCCGGTGACCTTTGGCAGGGGCA 240
 QY 241 CTCTTGAAGATCTCCGCTACCCCGGAGTCCCTGAGAGACCTGCTGAACCT 300
 Db 241 CTCTTGAAGATCTCCGCTACCCCGGAGTCCCTGAGAGACCTGCTGAACCT 300
 QY 301 GAGATCTGGGCCCCCTGAAACCGCTAGAACGATCTCTCAACTCCCGGCTGACGAC 360
 Db 301 GAGATCTGGGCCCCCTGAAACCGCTAGAACGATCTCTCAACTCCCGGCTGACGAC 360
 QY 361 CTTTGGCCGAGAGACCCCGGAGAAACCTCTGAGCTCTGAGGTGAGC 420
 Db 361 CTTTGGCCGAGAGACCCCGGAGAAACCTCTGAGCTCTGAGGTGAGC 420
 QY 421 AACCGACCTCAGAGAGCAGACCTAGACCCACCCCGGAGAGATGATGAGAT 480
 Db 421 AACCGACCTCAGAGAGCAGACCTAGACCCACCCCGGAGAGATGATGAGAT 480

QY 481 CCCTCAGCGCTTCTGTTCACAGGACATCTCCAGGACCCACGCGCTCTCCACCTGTGAT 540
 Db 481 CCCTCAGCGCTTCTGTTCACAGGACATCTCCAGGACCCACGCGCTCTCCACCTGTGAT 540
 QY 541 TCCCGGATTTCTCCCAATTTAGCTATCTCTTAAACCTCTTCTCATTCCCTCGGT 600
 Db 541 TCCCGGATTTCTCCCAATTTAGCTATCTCTTAAACCTCTTCTCATTCCCTCGGT 600
 QY 601 TTTATTTGAAACCCGTAAGGTGTGTTCTCAATTTCTGTCCTCTGAGATCCATA 660
 Db 601 TTTATTTGAAACCCGTAAGGTGTGTTCTCAATTTCTGTCCTCTGAGATCCATA 660
 QY 661 CTATGCTCAGATCGCGCGTCTTTTCTCTGACAGCTTAAGCTTCTCTACCTCGC 720
 Db 661 CTATGCTCAGATCGCGCGTCTTTTCTCTGACAGCTTAAGCTTCTCTACCTCGC 720
 QY 721 CTCAGGCTCGGAGCCGACCTTCCACCCGCTTCTCTGCGCGGAGTGTGAGG 780
 Db 721 CTCAGGCTCGGAGCCGACCTTCCACCCGCTTCTCTGCGCGGAGTGTGAGG 780
 QY 781 CAGGCTATGATCTGTGTTCTTCTGCACTGTGTGCGCGGAGGAGATATCACT 840
 Db 781 CAGGCTATGATCTGTGTTCTTCTGCACTGTGTGCGCGGAGGAGATATCACT 840
 QY 841 AGACAGCTGCTGCTTCATGAAACGAGAAATATATATGTTTCTTAA 891
 Db 841 AGACAGCTGCTGCTTCATGAAACGAGAAATATATATGTTTCTTAA 891

RESULT 2
 ABN60006
 ID ABN60006 standard; cDNA; 1473 BP.
 AC ABN60006;

XX 28-JUN-2002 (first entry)
 DE Novel human coding sequence SEQ ID NO: 417.
 XX

KW Human; anti-nausea; vulnary; anti-inflammatory; immunomodulator;
 KW anti-fertility; cerebroprotective; cytoskeletal; rheumatic; gene therapy;
 KW neuroprotective; anti-parasitosis; protein therapy; ESR;
 KW expressed sequence tag; gene; ss.

OS Homo sapiens.

PN WO200222660-A2.

XX 21-MAR-2002.

PF 10-SEP-2001; 2001MO-US026015.

PR 11-SEP-2000; 2000US-00659671.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;

DR WPI; 2002-292408/33.
 DR P-PSDB; ABB97593.

PT An isolated polynucleotide for treating diseases associated with its
 PT encoded polypeptide such as cancer and multiple sclerosis.

XX Claim 1; SEQ ID NO 417; 509pp; English.

XX The present invention provides the protein and coding sequences of 444
 CC novel human proteins. These were isolated from expressed sequences tags
 CC (ESTs). They can be used to stimulate cell growth, to regulate
 CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
 CC e.g. in burn treatment, to regulate the immune system e.g. to treat

multiple sclerosis, to regulate activin or inhibit e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a coding sequence of the invention

Sequence 1473 BP; 294 A; 491 C; 382 G; 306 T; 0 U; 0 Other;

Query Match 92.9%; Score 828; DB 6; Length 1473;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 878; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

13 CCAGAGGACCCAGACCTGAGCCAGCCAGCTTTGGGGCCAGTATAGCATATGCTC 72
585 CCAGAGGACCCAGACCTGAGCCAGCCAGCTTTGGGGCCAGTATAGCATATGCTC 644
73 AACTGAAAGCTCTGGGATCTGTGCTTTCCTGACACACAGAGGATCTCAGGAGC 132
645 AACTGAAAGCTCTGGGATCTGTGCTTTCCTGACACACAGAGGATCTCAGGAGC 704
133 GAGGGCCACCCCTCTACACCCGAGAGGACCGAAGAGAGGAGGCTCCCAACTTG 192
705 GAGGGCCACCCCTCTACACCCGAGAGGACCGAAGAGAGGAGGCTCCCAACTTG 764
193 CCTCAGGGGCCCCAGTCCCGGAGACCTTTGGCAGGGGACCCCTCTTTTGAAGAT 252
765 CCTCAGGGGCCCCAGTCCCGGAGACCTTTGGCAGGGGACCCCTCTTTGAAGAT 824
253 CCTCAGGGGCCCCAGTCCCGGAGACCTTTGGCAGAGACCTGCTGAAGTCTGAGCC 312
825 CCTCAGGGGCCCCAGTCCCGGAGACCTTTGGCAGAGACCTGCTGAAGTCTGAGCC 884
313 CCTGAACCCGCTTGAAGAGATCTCTCTCAACCTCCCGGCTGACGACCTTTGGCCGCA 372
885 CCTGAACCCGCTTGAAGAGATCTCTCTCAACCTCCCGGCTGACGACCTTTGGCCGCA 944
373 GAGAGGACCCAGAGGACCCGCTGAGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 432
945 GAGAGGACCCAGAGGACCCGCTGAGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1004
433 GAGAGGACCCAGAGGACCCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 492
1005 GAGAGGACCCAGAGGACCCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1064
493 TGTGTTCCAGGACATCTCAAGGACCCAGGCTCTCCACCTCTGATTCCTCCGTAATT 552
1065 TGTGTTCCAGGACATCTCAAGGACCCAGGCTCTCCACCTCTGATTCCTCCGTAATT 1124
553 CTTCGCCAATTAGCTATCTCTTAACCTCTTCTGATTCCTCCGCTTTTATTTGTAAC 612
1125 CTTCGCCAATTAGCTATCTCTTAACCTCTTCTGATTCCTCCGCTTTTATTTGTAAC 1184
613 CCGTAAAGTGTGTCTCAATATTTCTGCTCCCTCTGAGATCATACTTATGCTCTCAC 672
1185 CCGTAAAGTGTGTCTCAATATTTCTGCTCCCTCTGAGATCATACTTATGCTCTCAC 1244
673 ATGCGCCGTTTTTCTCTGACAGCTTAAGCTTACTCTTCACTGCTCCAGGCTCTG 732
1245 ATGCGCCGTTTTTCTCTGACAGCTTAAGCTTACTCTTCACTGCTCCAGGCTCTG 1304
733 GCGCCACCTTACCTCCACCGGGTCTTCTCCCGGAGGAGTCTGAGGAGGAGGAGTANGT 792
1305 GCGCCACCTTACCTCCACCGGGTCTTCTCCCGGAGGAGTCTGAGGAGGAGGAGTANGT 1364
793 ACTGTGTTCCCTTCTGACCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 852
1365 ACTGTGTTCCCTTCTGACCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1424
853 CTTCATGAAACGGAATAATTAATCATGTTTCTTAA 891
1425 CTTCATGAAACGGAATAATTAATCATGTTTCTTAA 1463

RESULT 3
ABK86967
ID ABK86967-standard; DNA; 2997 BP.
XX
AC ABK86967;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human CAN-1 deletion polymorphism genomic DNA.
XX
XX Human; antipsoriatic; chromosome 6; candidate coding sequence-1; CAN-1;
XX SEBK-1; STG; human leukocyte antigen C; HLA C; HLA Cw6; psoriasis; skin;
XX keratinocyte; chronic inflammatory dermatosis; erythroderma; seboretic;
XX guttate; pustular variant; Reiter's disease; hyperproliferation;
XX epidermis; differentiation; diagnosis; gene therapy; gene; ds; SNP;
XX single nucleotide polymorphism; deletion polymorphism.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX variation replace(11..12,CCAGA)
XX FT /*tag= a
XX FT /note= "Deletion polymorphism"
XX FT replace(114,T)
XX FT /*tag= b
XX FT /standard_name= "Single nucleotide polymorphism"
XX FT replace(361,A)
XX FT /*tag= c
XX FT /standard_name= "Single nucleotide polymorphism"
XX FT replace(550,A)
XX FT /*tag= d
XX FT /standard_name= "Single nucleotide polymorphism"
XX FT replace(966,G)
XX FT /*tag= e
XX FT /standard_name= "Single nucleotide polymorphism"
XX FT replace(1096,T)
XX FT /*tag= f
XX FT /standard_name= "Single nucleotide polymorphism"
XX FT replace(1196,A)
XX FT /*tag= g
XX FT /standard_name= "Single nucleotide polymorphism"
XX FT replace(1390,T)
XX FT /*tag= h
XX FT /standard_name= "Single nucleotide polymorphism"
XX FT 1481..2557
XX FT /*tag= i
XX FT /product= "CAN-1"
XX FT 1481..1535
XX FT /*tag= j
XX FT /number= 1
XX FT 1536..2201
XX FT /*tag= k
XX FT /number= 1
XX FT replace(1677,A)
XX FT /*tag= l
XX FT /standard_name= "Single nucleotide polymorphism"
XX FT replace(1875,T)
XX FT /*tag= m
XX FT /standard_name= "Single nucleotide polymorphism"
XX FT replace(1982,A)
XX FT /*tag= n
XX FT /standard_name= "Single nucleotide polymorphism"
XX FT replace(2016,C)
XX FT /*tag= o
XX FT /standard_name= "Single nucleotide polymorphism"
XX FT replace(2107,G)
XX FT /*tag= p
XX FT /standard_name= "Single nucleotide polymorphism"
XX FT 2202..2557
XX FT /*tag= q
XX FT /number= 2
XX FT replace(2393,T)
XX variation

FT	variation	replace(554,A)	
FT		/*tag= c	
FT	variation	/standard_name=	"Single nucleotide polymorphism"
FT		replace(1100,T)	
FT		/*tag= d	
FT	variation	/standard_name=	"Single nucleotide polymorphism"
FT		replace(1200,A)	
FT		/*tag= e	
FT	variation	/standard_name=	"Single nucleotide polymorphism"
FT		replace(1394,T)	
FT		/*tag= f	
FT	CDS	/standard_name=	"Single nucleotide polymorphism"
FT		1485..2561	
FT		/*tag= g	
FT		/product= "CAN-1"	
FT	exon	1485..1539	
FT		/*tag= h	
FT		/number= 1	
FT	intron	1540..2205	
FT		/*tag= i	
FT		/number= 1	
FT	variation	replace(1681,A)	
FT		/*tag= j	
FT	variation	/standard_name=	"Single nucleotide polymorphism"
FT		replace(1879,T)	
FT		/*tag= k	
FT	variation	/standard_name=	"Single nucleotide polymorphism"
FT		replace(1586,A)	
FT		/*tag= l	
FT	variation	/standard_name=	"Single nucleotide polymorphism"
FT		replace(2020,C)	
FT		/*tag= m	
FT	variation	/standard_name=	"Single nucleotide polymorphism"
FT		replace(2111,G)	
FT		/*tag= n	
FT	exon	/standard_name=	"Single nucleotide polymorphism"
FT		2206..2561	
FT		/*tag= o	
FT		/number= 2	
FT	variation	replace(2397,T)	
FT		/*tag= p	
FT	variation	/standard_name=	"Single nucleotide polymorphism"
FT		replace(2655,G)	
FT		/*tag= q	
FT	variation	/standard_name=	"Single nucleotide polymorphism"
FT		replace(2822,G)	
FT		/*tag= r	
FT	variation	/standard_name=	"Single nucleotide polymorphism"
FT		replace(2875,C)	
FT		/*tag= s	
FT	variation	/standard_name=	"Single nucleotide polymorphism"
XX			
PN	WO20024375-A2.		
XX			
PD	06-JUN-2002.		
XX			
PF	27-NOV-2001; 2001WO-US044506.		
XX			
PR	28-NOV-2000; 2000US-0253592P.		
XX			
PR	15-DEC-2000; 2000US-0256839P.		
XX			
PA	(CELL-) CELLTECH R & D INC.		
XX			
PI	Charmley P, Moss P, McEuen M;		
XX			
DR	WPI; 2002-508513/54.		
XX	P-PSDB; AAU79579.		
PT	Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation		
PT	and differentiation, and polynucleotides encoding the polypeptide, useful		
PT	for diagnosing or predicting susceptibility to psoriasis in individual.		
XX			
S5	Claim 18; Page 82-84; 95bp; English.		

CC	The invention discloses isolated candidate coding sequence-1 (CAN-1),
CC	SEBK-1,(not defined) and STG (not defined) polypeptides, and the
CC	polynucleotides encoding them. All three genes were identified due to
CC	their proximity to the human leukocyte antigen C (HLA C) locus on
CC	chromosome 6. The HLA CW6 allele is associated with psoriasis and as the
CC	three genes are expressed in normal skin and/or keratinocyte tissue, they
CC	may also have a role in psoriasis. Psoriasis is a chronic inflammatory
CC	dermatosis that is characterized by hyperproliferation of epidermal
CC	cells. Possible treatments against psoriasis involve the inhibition of
CC	movement of cells into the epidermis, or the inhibition of
CC	hyperproliferation or abnormal differentiation of keratinocytes, by the
CC	inhibition of the CAN-1, STG or SEBK-1 polypeptides binding to their
CC	binding partners. The polypeptides are useful for diagnosing or
CC	predicting the susceptibility to psoriasis in an individual, for
CC	ameliorating the symptoms and/or progression of psoriasis and for
CC	identifying agents useful for treating psoriasis or modulating the
CC	activity of the polypeptide. The polypeptides are also useful for
CC	enhancing the level of CAN-1, STG or SEBK-1 biological activity in a cell
CC	or tissue. The nucleic acid molecules are useful as hybridisation probes
CC	in diagnostic procedures (such as diagnosing the presence of psoriasis or
CC	the propensity to develop psoriasis) and for suppressing the expression
CC	of CAN-1 or STG gene (e.g., antisense inhibition, gene therapy).
CC	Antibodies, raised against the polypeptides, are useful for decreasing
CC	the level of CAN-1, STG or SEBK-1 biological activity in a cell. The
CC	sequence presented is the human candidate coding sequence-1 (CAN-1)
CC	genomic DNA
XX	
SQ	Sequence 3001 BP; 619 A; 786 C; 914 G; 682 T; 0 U; 0 Other;
Query Match	87.0%; Score 775; DB 6; Length 3001;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 775; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	117 AGGCATCMCAGGGCGAGAGGGGCCACCCCTCTCACACCACCGCAGAGAACCGAGAGAGGC 176
DB	2204 AGGCATCTCAGGCGAGGAGGGCCACCCCTCTCACACCACCGCAGAGAACCGAGAGAGGC 2263
OY	177 AGGCTCCCCCAATGTGCTCAGAGGCCCCGCCAGTCCC CGGTGACCTTTGCGCAGGGGACCC 236
DB	2264 AGGCTCCCCCAATGTGCTCAGAGGCCCCGCCAGTCCC CGGTGACCTTTGCGCAGGGGACCC 2323
OY	237 CCCTTCCTTTGAAGATCCTCCGCTACCCGSCCAGCGTGCTCCGTGAGAGACTGECCTGA 296
DB	2324 CCCTTCCTTTGAAGATCCTCCGCTACCCGSCCAGCGTGCTCCGTGAGAGACTGECCTGA 2383
OY	297 AACGTGAGTCTGGGCCCCCTGAACCGCCTAAAGGATCTCTCAACCTCCCGGCTGA 356
DB	2384 AACGTGAGTCTGGGCCCCCTGAACCGCCTAAAGGATCTCTCAACCTCCCGGCTGA 2443
OY	357 CGACCCATTGGCCGGCAGAGACCCCGAGCCCCCAGAAAACCCCTGGGCTCTCTGCCCCCTGAGGT 416
DB	2444 CGACCCATTGGCCGGCAGAGACCCCGAGCCCCCAGAAAACCCCTGGGCTCTCTGCCCCCTGAGGT 2503
OY	417 GGACAACCGAAGCTTAGAGAGAGCCAGACTAGACCAACCCCGGGAAGATACAGATTAATG 476
DB	2504 GGACAACCGAAGCTTAGAGAGAGCCAGACTAGACCAACCCCGGGAAGATACAGATTAATG 2563
OY	477 GAGTCCCTCAGCCGCTTCTGTTCACAGGACATCTCAAGGACCCACGCGCTCTCCACCTCTC 536
DB	2564 GAGTCCCTCAGCCGCTTCTGTTCACAGGACATCTCAAGGACCCACGCGCTCTCCACCTCTC 2623
OY	537 TGATTTCCCGGAGATTTCTTCCCAATTAGCTATCTCTTAAACCTCTTCCCTCATTCCTCT 596
DB	2624 TGATTTCCCGGAGATTTCTTCCCAATTAGCTATCTCTTAAACCTCTTCCCTCATTCCTCT 2683
OY	597 CGGTTTTATTTGAACCGTAAGGTGTGTCTCAATATTTTCTGTCCCTCTGAGATC 656
DB	2684 CGGTTTTATTTGAACCGTAAGGTGTGTCTCAATATTTTCTGTCCCTCTGAGATC 2743
OY	657 CATACTTAAGTCTCAATCGCCGCTTTTTCCTCTGACAGCTTAAGGCTACTCTCTCAAC 716
DB	2744 CATACTTAAGTCTCAATCGCCGCTTTTTCCTCTGACAGCTTAAGGCTACTCTCTCAAC 2803

```

QY 717 TCGGCTCCAGGCTCGGCCCCCACTACCTCCACCCGGTCTTCTGCGCCGCGGATGCT 776
DB 2804 TCGGCTCCAGGCTCGGCCCCCACTACCTCCACCCGGTCTTCTGCGCCGCGGATGCT 2863
QY 777 GGGGCAAGGCTAGTACTGTGTTCCCTTGCACCTGTGCGCGGCGAGAACTAT 836
DB 2864 GGGGCAAGGCTAGTACTGTGTTCCCTTGCACCTGTGCGCGGCGAGAACTAT 2923
QY 837 CAGTAGACAGCTGCTGCTCCATGAAACGGAATAATAATCATGTTTCTTAA 891
DB 2924 CAGTAGACAGCTGCTGCTCCATGAAACGGAATAATAATCATGTTTCTTAA 2978

RESULT 5
AAH45310
ID AAH45310 standard; DNA, 25235 BP.
AC AAH45310;
DT 01-OCT-2001 (first entry)
XX
DE Human SBEK1 DNA.
XX
KM Human; MHC S; major histocompatibility complex S; vulgar psoriasis;
KM diagnosis; primer; SBEK1; HCR; a-helix coiled-coil rod homologue;
KM polymorphism; de.
XX
OS Homo sapiens.
XX
FH Key
FT exon 1..420
FT intron /+tag= a
FT exon 421..1281
FT intron /+tag= b
FT exon 1282..1405
FT intron /+tag= c
FT exon 1406..1601
FT intron /+tag= d
FT exon 1602..1702
FT intron /+tag= e
FT exon 1703..2351
FT intron /+tag= f
FT exon 2352..2364
FT intron /+tag= g
FT exon 2365..6286
FT intron /+tag= h
FT exon 6287..6509
FT intron /+tag= i
FT exon 6510..10416
FT intron /+tag= j
FT exon 10417..10493
FT intron /+tag= k
FT exon 10494..14243
FT intron /+tag= l
FT exon 14244..14407
FT intron /+tag= m
FT intron 14408..14243
FT intron /+tag= n
FT exon 25190..25235
FT exon /+tag= o
XX
PN WO200142458-A1.
XX
PD 14-JUN-2001.
XX
PF 06-DEC-2000; 2000MO-JP008624.
XX
PR 06-DEC-1999; 99JP-00346867.
XX
PA (INOK/) INOKO H.
XX
PI Inoko H, Tamiya G;

```

```

XX WPI; 2001-381680/40.
DR
XX New primer DNA, useful for detecting vulgar psoriasis.
PT
XX Claim 1; Page 46-62; 106pp; Japanese.
PS
XX The invention relates to a method of diagnosing vulgar psoriasis using
CC primers based on the sequences of the human MHC S, SBEK1 and HCR genes.
CC By analysing the sequences of these genes in Japanese patients with
CC psoriasis and in normal subjects, it has been found that some of the
CC examined polymorphisms correlate significantly to the group of patients
CC with psoriasis. Vulgar psoriasis can therefore be diagnosed by analysing
CC these gene polymorphisms. The present sequence is the human SBEK1 gene
CC which was used to design primers for use in the invention
XX
SQ Sequence 25235 BP; 5967 A; 6703 C; 6487 G; 6078 T; 0 U; 0 Other;
Query Match 81.3%; Score 724; DB 4; Length 25235;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 774; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 117 AGGCATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 176
DB 1753 AGGCATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1812
QY 177 AGGCTCCCAACATGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 236
DB 1813 AGGCTCCCAACATGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1872
QY 237 CCTCTCTTGAAGATCTCTCCGCTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 296
DB 1873 CCTCTCTTGAAGATCTCTCCGCTACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1932
QY 297 AACTGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 356
DB 1933 AACTGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1992
QY 357 CGACCTTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 416
DB 1993 CGACCTTGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2052
QY 417 GGAACACGACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 476
DB 2053 GGAACACGACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2112
QY 477 GAGTCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 536
DB 2113 GAGTCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2172
QY 537 TGATTCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 596
DB 2173 TGATTCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2232
QY 597 CGGTTTATTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 656
DB 2233 CGGTTTATTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2292
QY 657 CATACTAGTCCGACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 716
DB 2293 CATACTAGTCCGACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2352
QY 717 TCGGCTCCAGGCTCGGCCCCCACTACCTCCACCCGGTCTTCTGCGCCGCGGATGCT 776
DB 2353 TCGGCTCCAGGCTCGGCCCCCACTACCTCCACCCGGTCTTCTGCGCCGCGGATGCT 2412
QY 777 GGGGCAAGGCTAGTACTGTGTTCCCTTGCACCTGTGCGCGGCGAGAACTAT 836
DB 2413 GGGGCAAGGCTAGTACTGTGTTCCCTTGCACCTGTGCGCGGCGAGAACTAT 2472
QY 837 CAGTAGACAGCTGCTGCTCCATGAAACGGAATAATAATCATGTTTCTTAA 891
DB 2473 CAGTAGACAGCTGCTGCTCCATGAAACGGAATAATAATCATGTTTCTTAA 2527

```


RESULT 6
ABQ75680 standard; DNA, 55050 BP.
XX ABQ75680;
AC ABQ75680;
XX 11-NOV-2002 (first entry)
DT 11-NOV-2002 (first entry)
XX Human SEBK1 consensus genomic DNA.
DE Human SEBK1; chromosome 6p21; inflammatory disease; antiinflammatory;
KM Human; SEBK1; gene therapy; gene; ds.
XX antiporiatic; gene therapy; gene; ds.
OS Homo sapiens.
XX MO200264831-A2.
PN 22-AUG-2002.
PD 13-FEB-2002; 2002MO-GB000653.
PP 13-FEB-2001; 2001GB-00003514.
XX 13-FEB-2001; 2001GB-00003514.
XX (OXAG-) OXAGEN LTD.
PA Iench NJ, Allen MJ, Nicholls RK;
PI WPI; 2002-667013/71.
XX Polymorphisms in the SEBK1 gene and polymucleotides encoding the SEBK1
PT gene, for treating, diagnosing or determining susceptibility to SEBK1
PT mediated disease, e.g. inflammatory disease such as psoriasis.
XX
PS Claim 4; Fig 2; 69pp; English.
XX
CC The present invention describes a polymucleotide (I) comprising: (a) a
CC nucleic acid sequence (II) encoding the SEBK1 gene; (b) a nucleic acid
CC sequence (III) encoding a fragment of the SEBK1 gene; or (c) a nucleic
CC acid sequence (IV) that hybridizes under stringent conditions to the
CC polymucleotide of (II) or (III). (I) has antiinflammatory and
CC antiporiatic activities and can be used in gene therapy. The alleles of
CC one or more polymorphisms in the SEBK1 gene can be used for the
CC manufacture of a medicament for the diagnosis and treatment of SEBK1
CC mediated disease. SEBK1 protein fragments are useful in diagnostic,
CC prognostic or therapeutic methods, or as research tools in drug
CC screening. Human SEBK1 is located to chromosome 6p21. The present
CC sequence represents a human SEBK1 nucleotide sequence
XX
SQ Sequence 55050 BP, 13076 A; 14198 C; 14560 G; 13197 T; 0 U; 19 Other;
Query Match 81.3%; Score 724; DB 6; Length 55050;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 774; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 117 AGGCATCTCAGGAGCGAGGCGACCCCTCTCACCACCGGAGAGACCGGAGAGGC 176
DB 27098 AGGCATCTCAGGAGCGAGGCGACCCCTCTCACCACCGGAGAGACCGGAGAGGC 27157
QY 177 AGGCTCCCAACANTGCTCAGGAGGCGCGCCGAGTCCCGGGTGAACCTTGGCCAGGGGCAAC 236
DB 27158 AGGCTCCCAACANTGCTCAGGAGGCGCGCCGAGTCCCGGGTGAACCTTGGCCAGGGGCAAC 27217
QY 237 CCCTCTCTTGAAGATCTCCGCTACCGCGCCGAGTCTCTCTGAGAGACTGCTCTGA 296
DB 27218 CCCTCTCTTGAAGATCTCCGCTACCGCGCCGAGTCTCTCTGAGAGACTGCTCTGA 27277
QY 297 AACTGAGTCTGGCCCTTGAACCGCTTGAACGAGATCTCTCAACCTCCCGGCTGA 356
DB 27278 AACTGAGTCTGGCCCTTGAACCGCTTGAACGAGATCTCTCAACCTCCCGGCTGA 27337
QY 357 GACCCCTTGGCGGCGAGAGACCCGAGCCCGGAGAAACCCCTGGCTCTCTGAGGT 416

DB 27338 GACCCCTTGGCGGCGAGAGACCCGAGCCCGGAGAAACCCCTGGCTCTCTGAGGT 27397
QY 417 GAGCAACCGACTCTCAGGAGAGCGCAGACTTACACCCACCCCGGAGAGATGATATG 476
DB 27398 GAGCAACCGACTCTCAGGAGAGCGCAGACTTACACCCACCCCGGAGAGATGATATG 27457
QY 477 GAGTCCCTCAGGCGGCTCTGCTCCAGGAGCTTCCAGGAGACCGACGCGCTCTCCACCTC 536
DB 27458 GAGTCCCTCAGGCGGCTCTGCTCCAGGAGCTTCCAGGAGACCGACGCGCTCTCCACCTC 27517
QY 537 TGAATCCCGTGAATCTTCCCAATTAGCCTTATCTCTTAAACCTTCTCATTCCT 596
DB 27518 TGAATCCCGTGAATCTTCCCAATTAGCCTTATCTCTTAAACCTTCTCATTCCT 27577
QY 597 CGGTTTATCTGAACCGCTTGAAGGTGTCTTCAATATTTCTGTCCCTCTGAGATC 656
DB 27578 CGGTTTATCTGAACCGCTTGAAGGTGTCTTCAATATTTCTGTCCCTCTGAGATC 27637
QY 657 CATACTAGTCCACATCGGCGGTTTCTCTGACAGGCTTAAAGCTTACTGCTTACC 716
DB 27638 CATACTAGTCCACATCGGCGGTTTCTCTGACAGGCTTAAAGCTTACTGCTTACC 27697
QY 717 TCGCCTCCAGGCTCGGCGCCACCTACCTCCACCGGCTTCTGCGCGGAGATGCT 776
DB 27698 TCGCCTCCAGGCTCGGCGCCACCTACCTCCACCGGCTTCTGCGCGGAGATGCT 27757
QY 777 GGGGAGGAGGCTTATGTAATGTGTCTTCTGCGACCTGTGTGGCGGAGAGACTAT 836
DB 27758 GGGGAGGAGGCTTATGTAATGTGTCTTCTGCGACCTGTGTGGCGGAGAGACTAT 27817
QY 837 CAGTACGACCTCTGCTTCCATGAAGAAACGAAATAATATGTTTCTTAA 891
DB 27818 CAGTACGACCTCTGCTTCCATGAAGAAACGAAATAATATGTTTCTTAA 27872
RESULT 7
ACH72505
ID ACH72505 standard; DNA, 565 BP.
XX
AC ACH72505;
XX
DT 29-JUL-2004 (first entry)
XX
DB Human genome derived single exon probe #5700.
XX
KM Human; probe; ss; gene expression; single exon probe; microarray;
KM alternative splicing event; genomic alteration.
XX
OS Homo sapiens.
XX US2003194704-A1.
PN 16-OCT-2003.
PD 03-APR-2002; 2002US-00029386.
PP 03-APR-2002; 2002US-00029386.
XX
PR 03-APR-2002; 2002US-00029386.
XX
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
XX
PI Penn SG, Rank DR, Hanzel DK;
XX
DR WPI; 2004-119264/12.
XX
PT New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX
PS Claim 15; SEQ ID NO 5700; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subcription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above). The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that convey their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030194704

SQ Sequence 565 BP; 99 A; 227 C; 112 G; 127 T; 0 U; 0 Other;

Query Match	62.28; Score 554; DB 12; Length 565;
-------------	--------------------------------------

Matches 554; Conservative 0; Mismatches 0; Indels 0; Gaps. 0;

235 CCCCTCTTGAAGATCCGCGCTACCGCGCCGAGTGTCCCTGGAGAGACCTGCT 294

Db 1 CCCCCTCTTTGAGATCCTCCGCTACCCGCCAGTCGTCCTTGAGAGACCTGCT 60 .

295 GAACTGGAGTCTGGCCCCCTGAACCGCCTAGAACGATCCTCCTCAACCTCCCGGCT 354

Db 61 GAACTGGAGTCTGGCCCCCTGAACCGCCTAGAACGGATCCTCCTCAACCTCCCGGCCT 120

355 GACGACCTTGGCCGGCAGGACCCCAAGAAACCCCTGGCTCCTGCCCTGAG 414

Db 121 GACGACCCCTTGGCCGCGAGGACCCCGCCCGAGAAACCCCTGGCTCCTGCCCCCTGAG 180

415 GTGGACAACCGACTCAGGAGGAGCCAGACTAGACCCACCCCGGAGAGTACAGATAA 474

Db 181 GTGACAAACCGACTCAGGAGGAGCCAGACTAGACCCACCCCGGAGAGTACAGATA 240

475 TGGAGTCCCCCTCAGCCGTTCTGTTCACGCACTCCAGGCACCACGCCCTCTCCACCC 534

D_b 241 TGGAGTCCCTCAGCCGTTCTGTTCACGCATCTCCAGGCCACCACGCCCTCTCCACC 300

535 TCTGATTCCCGTGAATTCTTCCCAATTAGCCATCTCCTTAAACCTCTTCCCTCATTCC 594

Db 301 TCTGATTCCTCCGATTCCTCCCAATTAGCCTATCTCCTTAAACCTCTTCCCTCATTC 360

595 CTGGTTTATTCTGAACCGTAGGTGGTGTCTCATATTTCCCTGCCCTCTGAGA 654

Db 361 CTCGGTTTATTCTGAACCCGTAAGGTGGTGTCTCATATAITTCCTGTCCCTCCTGAGA 420

655 TCCATACCTTAGTCCTCACATCGCCGGTTTTTCTCCTGACAGCCTAAGCCTACTCTCCTA 714

Accession	Sequence	Position
Db	421 TCCATACCTTAGTCCTCCACATCGCCCGTTTTTTCCTGACAGCCCTAAGCTACTCTCCCTA	480
QY	715 CCTGGCCTTCCAGGCTCTGGGCCCCCAGCTACTCTCCCAACCGGCTCTTCTGCGCGGGGCGCATGG	774
Db	481 CCTCGCCTCCAGGCTCTGGGCCCCCAGCTACTCTCCACCGCGTCTTCTGCGCGGGCGATCG	540
QY	775 CTGGGGCAAGGGCTTA	788
Db	541 CTGGGGCAAGGGCTTA	554

1

ACH86315

XX XX

XX

XXIX

XX

KW alternative splicing event; genomic alteration.

OS Homo sapiens.

PN US2003194704-A1
yy

PD 16-OCT-2003
xy

PF 03-APR-2002; 2002US-00029386.
YY

PR 03-APR-2002; 2002US-00029386.
XY

PA	(PENN/)	PENN S G.
PA	(PANK/)	PANK D P

PA (HANZ/) HANZEL D K.
XY

PI	Penn SG,	Rank DR,	Hanzel DK;
XY			

DR WPI; 2004-119264/12.
XY

PT New human genome-derived single exon nucleic acid probes useful for human gene expression analysis for identifying or characterizing alternative

PT splicing events, for assessing genomic alterations or as tools for
PT surviving tissues

PS CJaim 1: SEO TD NO 19510: 80pm: Eng1:gh
XX

CC The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridises under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subcription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying

CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
CC
XX
SQ Sequence 157 BP; 38 A; 64 C; 38 G; 17 T; 0 U; 0 Other;
Query Match 17.6%; Score 157; DB 12; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.1e-66;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 318 ACCGCTAGAACGATCTCTCAACCTCCCGGCTGACGACCTTGCCGACGACC 377
DB 1 ACCGCTAGAACGATCTCTCTCACTCCCGGCTGACGACCTTGCCGACGACC 60
QY 378 CCAGCCCCCAGAAAACCCCTGCTCTCTGCTGCTGAGTGAGACACCGACTCAGAGGA 437
DB 61 CCAGCCCCCAGAAAACCCCTGCTCTCTGCTGCTGAGTGAGACACCGACTCAGAGGA 120
QY 438 GCCAGACTAGACCCACCCGGGAGAGTACAGATA 474
DB 121 GCCAGACTAGACCCACCCGGGAGAGTACAGATA 157

RESULT 9
ABN32329
ID ABN32329 standard; DNA; 60 BP.
AC ABN32329;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:5077.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001MO-IB001903.
XX
PR 28-JUL-2000; 2000US-0221607P.
XX
PR 02-MAY-2001; 2001US-0287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
PI WPI; 2002-257383/30.
XX
DR
XX
PT New oligonucleotide libraries comprising oligonucleotides which
XX selectively hybridize to mRNAs transcribed from a transcription unit of a
XX genome, useful for detecting tissue-, pathology-, and developmental-
XX specific genes.
XX
PS Example 1; SEQ ID NO 5077; 47bp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the (sub-
XX)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises several
XX oligonucleotides, each capable of hybridising selectively to a set of

CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at http://pub.wipo.int/pub/published_pct_sequences
CC
XX
SQ Sequence 60 BP; 11 A; 25 C; 5 G; 19 T; 0 U; 0 Other;
Query Match 6.7%; Score 60; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 6.2e-19;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 522 GCCCTTCACACCTGATTCCTCCGTAATTCCTCCCAATTAGCTATCTCTTAACC 581
DB 1 GCCCTTCACACCTGATTCCTCCGTAATTCCTCCCAATTAGCTATCTCTTAACC 60

RESULT 10
ABZ00541
ID ABZ00541 standard; DNA; 50 BP.
AC ABZ00541;
XX
DT 09-JAN-2003 (first entry)
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 532.
XX
XX
KW T7; leukocyte; gene expression profiling; allograft rejection;
XX atherosclerosis; congestive heart failure; systemic lupus erythematosus;
XX rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
XX ss.
XX
OS Homo sapiens.
XX
PN WO200257414-A2.
XX
PD 25-JUL-2002.
XX
PF 22-OCT-2001; 2001MO-US047856.
XX
XX
PR 20-OCT-2000; 2000US-0241994P.
XX
PR 08-JUN-2001; 2001US-0296764P.
XX
PA (BIOC-) BIOCARDIA INC.
XX
XX
PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX
PI Ly N, Woodward R, Quettermous T, Johnson F;
XX
XX
DR WPI; 2002-636525/68.
XX
XX
PT New system for leukocyte expression profiling, diagnosing a disease, or
XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX or congestive heart failure, comprises diagnostic oligonucleotides.
XX
XX
PS Claim 1; Page 342; Opp; English.
XX
XX The invention relates to a system for detecting gene expression, which
XX comprises one or two isolated DNA molecules that detect expression of a
XX gene, where the gene corresponds to any of 8143 oligonucleotides
XX (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful

CC for leukocyte expression profiling. It is particularly useful for
 CC diagnosing a disease, monitoring (rate of) progression of a disease,
 CC predicting therapeutic outcome, determining prognosis for a patient,
 CC predicting disease complications in an individual or monitoring response
 CC to treatment in an individual. The diseases include cardiac allograft
 CC rejection, kidney allograft rejection, liver allograft rejection,
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
 CC
 SQ Sequence 50 BP; 15 A; 13 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 5.6%; Score 50; DB 6; Length 50;
 Best Local Similarity 100.0%; Pred. No. 5.2e-14;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 820 CCGCGCGCAGGAACTATCAGTAGACAGCTGCTCTTCATGAAACGGAAA 869
 Db 1 CCGCGCGCAGGAACTATCAGTAGACAGCTGCTCTTCATGAAACGGAAA 50

RESULT 11
 AAC23697/c
 ID AAC23697 standard; cDNA; 204 BP.

XX AAC23697;
 AC
 XX 06-OCT-2000 (first entry)
 DT
 XX
 XX Human secreted protein 5' EST, SEQ ID NO: 27772.

KW Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KM gene therapy; chromosome mapping; ss.

XX Homo sapiens.
 OS
 XX BP1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (GEST) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

DR WPI; 2000-500381/45.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 1; SEQ ID NO 27772; 71pp + Sequence Listing; English.

CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
 CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
 CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
 CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors

XX Sequence 204 BP; 55 A; 75 C; 50 G; 24 T; 0 U; 0 Other;

XX Query Match 2.9%; Score 26; DB 3; Length 204;

Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 744 CTCACACCGGCTCTTCCTGCGCGCGC 769
 Db 26 CTCACACCGGCTCTTCCTGCGCGCGC 1

RESULT 12
 ABR86968
 ID ABR86968 standard; DNA; 21 BP.

XX ABR86968;

XX 24-SEP-2002 (first entry)

DE PCR primer, DMO 9299, used to amplify human CAN-1 cDNA.

XX Human; antipsoriatic; chromosome 6; candidate coding sequence-1; CAN-1;
 KM SEER-1; STG; human leukocyte antigen C; HLA C; HLA Cw6; psoriasis; skin;
 KM keratinocyte; chronic inflammatory dermatosis; erythroderma; seborethic;
 KM guttate; pustular variant; Reiter's disease; hyperproliferation;
 KM epidermis; differentiation; diagnosis; gene therapy; PCR; primer; ss;
 KM DMO 9299.

XX Homo sapiens.

XX MO200244375-A2.

XX 06-JUN-2002.

XX 27-NOV-2001; 2001WO-US044506.

XX 28-NOV-2000; 2000US-0253592P.

XX 15-DEC-2000; 2000US-0256839P.

XX (CELL-) CELLTech R & D INC.

XX Charley P, Moss P, Mceuen M;

XX WPI; 2002-508513/54.

XX Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation
 PT and differentiation, and polynucleotides encoding the polypeptide, useful
 PT for diagnosing or predicting susceptibility to psoriasis in individual.
 XX Example 2; Page 44; 95pp; English.

XX The invention discloses isolated candidate coding sequence-1 (CAN-1),
 CC SEER-1 (not defined) and STG (not defined) polypeptides, and the
 CC polynucleotides encoding them. All three genes were identified due to
 CC their proximity to the human leukocyte antigen C (HLA C) locus on
 CC chromosome 6. The HLA Cw6 allele is associated with psoriasis and as the
 CC three genes are expressed in normal skin and/or keratinocyte tissue, they
 CC may also have a role in psoriasis. Psoriasis is a chronic inflammatory
 CC dermatosis that is characterised by hyperproliferation of epidermal
 CC cells. Possible treatments against psoriasis involve the inhibition of
 CC movement of cells into the epidermis, or the inhibition of
 CC hyperproliferation or abnormal differentiation of keratinocytes, by the
 CC inhibition of the CAN-1, STG or SEER-1 polypeptides binding to their
 CC binding partners. The polypeptides are useful for diagnosing or
 CC predicting the susceptibility to psoriasis in an individual, for
 CC ameliorating the symptoms and/or progression of psoriasis and for
 CC identifying agents useful for treating psoriasis or modulating the
 CC activity of the polypeptide. The polypeptides are also useful for
 CC enhancing the level of CAN-1, STG or SEER-1 biological activity in a cell
 CC or tissue. The nucleic acid molecules are useful as hybridisation probes
 CC in diagnostic procedures (such as diagnosing the presence of psoriasis or
 CC the propensity to develop psoriasis) and for suppressing the expression
 CC of CAN-1 or STG gene (e.g. antisense inhibition, gene therapy).
 CC Antibodies, raised against the polypeptides, are useful for decreasing
 CC the level of CAN-1, STG or SEER-1 biological activity in a cell. The
 CC sequence presented is the PCR primer, DMO 9299, used to amplify human

CC candidate coding sequence-1 (CAN-1) cDNA
XX Sequence 21 BP; 4 A; 10 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 2.4%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 GACTCAGCCGACCCGACTTT 45
DB 1 GACTCAGCCGACCCGACTTT 21

RESULT 13
ADB58427/c
ID ADB58427 standard; DNA; 1315 BP.

XX ADB58427;

XX 04-DEC-2003 (first entry)

XX Toxicity-related gene, SEQ ID 3453.

XX Toxic; toxin; gene expression profile; hepatotoxicity; liver;

KM drug screening; toxicity assay; ds.

XX Unidentified.

XX WO2003064624-A2.

XX 07-AUG-2003.

XX 31-JAN-2003; 2003WO-US003194.

XX 31-JAN-2002; 2002US-00060087.

XX 15-MAR-2002; 2002US-0364045P.

XX 15-MAR-2002; 2002US-0364055P.

XX 30-DEC-2002; 2002US-0436643P.

XX (GENE-) GENE LOGIC INC.

XX Mendrick D, Porter M, Johnson K, Higgs B, Caastle A, Elashoff M;

XX WPI; 2003-689530/65.

XX Predicting a toxic effect of a compound, useful in identifying toxicity

XX markers in liver tissues or cells for drug screening and toxicity assays,

XX comprises preparing gene expression profile of tissue or cells exposed to

XX the compound.

XX Claim 1; SEQ ID NO 3453; 1156bp; English.

XX The present invention relates to a method for predicting a toxic effect

XX of a compound. The method comprises preparing a gene expression profile

XX of a tissue or cell sample exposed to the compound, and comparing the

XX gene expression profile to a database comprising SEQ ID 1-4925, where

XX differential expression of the gene indicates at least one toxic effect.

XX The method is useful for predicting or the progression of a toxic effect

XX of a compound, predicting hepatotoxicity or the progression of a toxic effect

XX progression of a toxic response, predicting the cellular pathways that a

XX compound modulates in a cell, and identifying an agent that modulates at

XX least one activity of a protein. The method and compositions of the

XX present invention using a database of genes having liver toxin-induced

XX differential expression, are useful in identifying toxicity markers in

XX liver tissues or cells for drug screening and toxicity assays. Note: The

XX sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1315 BP; 251 A; 384 C; 344 G; 336 T; 0 U; 0 Other;

XX Query Match 2.4%; Score 21; DB 10; Length 1315;

Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 TGGCCGCGAGACCCGAGCCC 384
DB 210 TGGCCGCGAGACCCGAGCCC 190

RESULT 14
AAV13900/c
ID AAV13900 standard; DNA; 229 BP.

XX AAV13900;

XX 18-JUN-1998 (first entry)

XX Fragments of the cDNA encoding c-mpl.

XX Driver DNA sequence; subtractive amplification; amplification; RNA;

KM selective amplification; diagnosis; genetic disease; mutation;

XX thrombopoietin receptor; c-mpl; ss.

XX Unidentified.

XX WO9741260-A2.

XX 06-NOV-1997.

XX 29-APR-1997; 97WO-US007253.

XX 29-APR-1996; 96US-00639763.

XX (GENE-) GENESCAPE INC.

XX Malek LT, Sooknunan RR;

XX WPI; 1998-086521/08.

XX Subtractive amplification method - useful in the diagnosis of genetic

XX disease, mutation or variation.

XX Example 2; Page 77; 111pp; English.

XX The present sequence represents nucleotides 29 to 197 of the cDNA of

XX thrombopoietin receptor (c-mpl). It was produced using primers AAV13887-

XX 88. The present sequence was ligated into the plasmid pCMT, which is used

XX for the preparation of tester RNA sequences from c-mpl. It can be used

XX for in vitro transcription with T7 polymerase to generate RNA that can be

XX amplified using primers AAV13893-94. The method of the invention,

XX subtractive amplification, is used to preferentially amplify target RNA

XX relative to non-target RNA from a test sample of RNA. It comprises

XX contacting the sample with driver sequences complementary to the non-

XX target RNA under conditions suitable for hybridisation, extending a

XX nucleic acid primer using the target RNA as a template to form a DNA

XX template complementary to at least a portion of the target RNA, extending

XX the DNA template using an annealed promoter template to form extended

XX complementary DNA and transcribing the extended DNA template to form

XX synthetic target RNA. The method is used for the selective amplification

XX of an RNA target sequence from a mixed RNA sample. This may be applied to

XX the diagnosis of genetic disease, mutation or variation

XX Sequence 229 BP; 51 A; 69 C; 54 G; 55 T; 0 U; 0 Other;

XX Query Match 2.2%; Score 20; DB 2; Length 229;

XX Best Local Similarity 100.0%; Pred. No. 29;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 GCTCCTGGGGATCCTGATCC 100
DB 158 GCTCCTGGGGATCCTGATCC 139

RESULT 15

```

AAC72265
ID AAC72265 standard; DNA; 289 BP.
XX
AC AAC72265;
XX
DT 09-FEB-2001 (first entry)
XX
DE Single nucleotide polymorphism containing sequence #698.
XX
KM Single nucleotide polymorphism; SNP; human; genetic disease;
XX disease susceptibility; cardiovascular system; endocrine system;
XX neurological system; forensic testing; paternity testing; ds.
XX
OS Homo sapiens.
XX
PN WO200058519-A2.
XX
PD 05-OCT-2000.
XX
PF 30-MAR-2000; 2000MO-US008440.
XX
PR 31-MAR-1999; 99US-0127248P.
XX
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (AFfy-) AFFYMETRIX INC.
XX
PI Altschuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;
XX Lipshutz RJ, Patil N, Sklar P;
XX
DR WPI; 2000-611722/58.
XX
PT Nucleic acid selected from one of 106 genes comprising single nucleotide
XX polymorphisms, allele-specific oligonucleotides to the genes are useful
XX for phenotypic correlations, forensics, paternity testing, medicine and
XX genetic analysis.
XX
PS Claim 1; Fig 5; 214pp; English.
XX
CC The present invention is concerned with a number of human single
XX nucleotide polymorphisms (SNPs) which the inventors identified in human
XX genes. These SNPs can be used in disease diagnosis and prediction of an
XX individual's susceptibility to disease, in forensic and paternity testing
XX and in genetic mapping. In particular, the SNPs of the invention can be
XX used to diagnose susceptibility to diseases of the cardiovascular,
XX endocrine and neurological systems, such as coronary artery disease,
XX schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
XX diseases. Note: The degenerate codon within the sequence represents the
XX position of an SNP, for example the letter S represents a polymorphism
XX where the nucleotide may be C or G
XX
SQ Sequence 289 BP; 62 A; 73 C; 92 G; 61 T; 0 U; 1 Other;
XX
Query Match 2.2%; Score 20; DB 3; Length 289;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 81 GCTCTGGGATCTGCTCC 100
DB 174 GCTCTGGGATCTGCTCC 193

```

Search completed: January 11, 2005, 09:34:11
 Job time : 543 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 11, 2005, 09:13:15 : Search time 3418 Seconds
(without alignments)
9499.064 Million cell updates/sec

Title: US-09-994-365-1

Sequence: 1 ccccttgggtccacgca.....taaaatcatgtctcttaa 891

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 1821965908 residues

Word size : 0

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	305	34.2	419	2	BF513178 UT-H-BW1-
C 2	201	22.6	336	1	AT150762 qc06e04.x
C 3	174	19.5	243	8	AQ357151 C17B1-E1-
C 4	129	14.5	372	8	AQ136453 HS_3040_B
C 5	77	8.6	763	8	AF057073 AF057073
C 6	38	4.3	332	1	AA763309 vV98h03.x
C 7	38	4.3	361	1	AA168568 ms31c08.x
C 8	38	4.3	379	1	AA791103 vV91a02.x
C 9	38	4.3	416	9	CG481452 OST13885
C 10	38	4.3	422	9	AI596929 vJ46e11.y
C 11	38	4.3	442	9	CG487403 OST22893
C 12	38	4.3	451	1	AA798896 vV94e08.x
C 13	38	4.3	459	8	CG484009 OST17807
C 14	38	4.3	489	8	BH098389 RPCT-24-3
C 15	38	4.3	562	1	AA530301 vJ46e11.x
C 16	38	4.3	669	9	CG484609 OST18617
C 17	26	2.9	322	9	CG474695 OST2738 M
C 18	26	2.9	383	2	AW315342 12593 MAR
C 19	26	2.9	395	9	CG528207 OST107284
C 20	26	2.9	695	5	EX118051 BX118051
C 21	25	2.8	283	9	CG474588 OST2539 M
C 22	25	2.8	386	9	CG474680 OST2720 M
C 23	25	2.8	415	1	AA126588 z117f08.x
C 24	25	2.8	475	9	CG473878 OST1668 M

25	2.7	593	7	CF765720	CF765720 C86001471
26	2.7	634	7	CF764947	CF764947 C86003088
27	2.6	454	24	BF902421	BF902421 CM1-NT024
28	2.5	579	8	AZ336625	AZ336625 IM0067C05
C 29	2.4	431	2	AW342146	AW342146 GENE8732
C 30	2.4	480	8	AQ334387	AQ334387 HS_5001_B
C 31	2.4	519	2	AW761913	AW761913 UR51d02.y
C 32	2.4	588	9	CL590154	CL590154 OB_Ba009
C 33	2.4	736	9	CL562924	CL562924 OB_Ba002
C 34	2.4	786	9	CGS04A37	AL281378 Tetradon
C 35	2.4	899	1	AL555610	AL555610 AL555610
C 36	2.4	927	3	CR709529	CR709529 Tetradon
C 37	2.4	993	9	CNS03Q9H	AL255662 Tetradon
C 38	2.2	139	8	AZ133627	AZ133627 RPCT-23-1
C 39	2.2	302	2	BB229733	BB229733 BB229733
C 40	2.2	337	4	BI042160	BI042160 MR4-NT014
C 41	2.2	340	9	CE623904	CE623904 L19T-g88-
C 42	2.2	348	2	BB793764	BB793764 BB793764
C 43	2.2	418	2	BF057445	BF057445 7K44a05.x
C 44	2.2	418	7	R80330	R80330 Y196B03.x1
C 45	2.2	437	2	AW426796	AW426796 61561 MAR

ALIGNMENTS

RESULT 1
BF513178/c
LOCUS
DEFINITION
UI-H-BW1-am]-d-04-0-UI.s1 NCI CGAP Sub7 Homo sapiens cDNA clone
IMAGE:3070111 3', mRNA sequence.
ACCESSION
BF513178
VERSION
BF513178.1 GI:11598357
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 419)
NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
Tumor Gene Index
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
JOURNAL
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:
NCI CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/www.bio.11nl.gov/bdtp/image/image.html
www-bio.11nl.gov/bdtp/image/image.html
Seq primer: M13 Forward
POLYA=yes.
FEATURES
source
1..419
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3070111"
/lab_host="DH10B (Life Technologies)"
/clone_1lb="NCI CGAP Sub7"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; NCI CGAP Sub7
is a subtracted library derived from NCI CGAP Sub6. The
NCI CGAP Sub7 library had 12 million recombinants. A
single-stranded DNA preparation of NCI CGAP Sub6 was used
as a tracer in a subtractive hybridization with a driver
comprising: the IMAGE pool (NCI CGAP Kid3 pool 1 LLM
3334-3337, 3682-3683, 3798-3803 (IMAGE Clones)
132376-132391, 1456008-1456775, 1500552-1502855);
NCI CGAP Kid3 pool 1 LLM 3338-3342, 3722-3725, 3776-3778
(IMAGE Clones) 1323912-1325831, 1471368-1472903,

1492104-1493255); NCI CGAP L45 pool 1 L1AM 3575-3582, 3851-3854 (IMAGE Clonoids 1414920-1417991, 1520904-1522439); NCI CGAP GC4 pool 1 L1AM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clonoids 1257096-1258631, 1469064-1470981, 1475992-1476743); NCI CGAP Pr22 pool 1 L1AM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonoids 985608-986759, 1101192-1101959, 1217928-1220615); NCI CGAP Colo pool 1 L1AM 2644-2653, 2871-2872 (IMAGE Clonoids 1057416-1061255, 1144584-1145351). (6% of the driver population), plus a pool of 3,840 arrayed clones from NCI CGAP Sub1 (IMAGE Clonoids 2708616-2710535) and NCI CGAP Sub2 (IMAGE Clonoids 2710536-2712455) (4% of the driver population), plus a pool of 11,136 clones from NCI CGAP Sub3 (IMAGE Clonoids 2712456-2723591) (10% of the driver population), plus a pool of 5,472 clones from NCI CGAP Sub4 (IMAGE Clonoids 2723592-2729326) (40% of the driver population), plus a pool of 4032 clones from NCI CGAP Sub6 (IMAGE Clonoids 2728969-2733190) (40% of the driver population). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806. TAG_TISSUE=ovary TAG_LIB=NCI CGAP_Ov18 TAG_SEQ=GCACAC"]

ORIGIN

Query Match 34.2%; Score 305; DB 2; Length 419;
Best Local Similarity 99.5%; Pred. No. 1.3e-148;
Matches 405; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

465 GTACAGATTAATGAGATCCCTCCAGCCGTTGTTCCAGGACATCTCAGGACCCAGCC 524
419 GTACAGATTAATGAGATCCCTCCAGCCGTTGTTCCAGGACATCTCAGGACCCAGCC 360

525 CTCTCCACCTCTGATTCCTCCGATTTCTTCCCAATTTAGCTATCTCTTAACTCT 584
359 CTCTCCACCTCTGATTCCTCCGATTTCTTCCCAATTTAGCTATCTCTTAACTCT 300

585 TCCCTATTCCTCGGTTTATTTCTGAACCGGTAAGGAGTCTCAATTTCTCTGTC 644
299 TCCCTATTCCTCGGTTTATTTCTGAACCGGTAAGGAGTCTCAATTTCTCTGTC 240

645 CTCTCTGAGATCAATTAATGATCTCAATGAGCCGTTTCTCTGAGAGCTTAAGCC 704
239 CTCTCTGAGATCAATTAATGATCTCAATGAGCCGTTTCTCTGAGAGCTTAAGCC 180

705 TACTCTCTACCTCGGCTCCAGGCTTGGGCTCCAGCTTCCAGCCGCTTCTGTC 764
179 TACTCTCTACCTCGGCTTCCAGGCTTGGGCTCCAGCTTCCAGCCGCTTCTGTC 120

765 CGCGCATGCTGGGCGAGGCTAGTGTGTTCCCTTGTGCACTGGTGGCGGG 824
119 CGCGCATGCTGGGCGAGGCTAGTGTGTTCCCTTGTGCACTGGTGGCGGG 60

825 GCGAGGAACTATAGTAGACAGCTGCTCTTCATGAAGCAAGAAA 871
59 GCGAGGAACTATAGTAGACAGCTGCTCTTCATGAAGCAAGAAA 13

RESULT 2
A1150762/c 336 bp mRNA linear EST 30-SBP-1998
LOCUS A1150762
DEFINITION qc06e04.x1 Soares fetal heart NBH19W Homo sapiens cDNA clone
IMAGE:1708830 3', mRNA sequence.
ACCESSION A1150762
VERSION A1150762.1 GI:3679231
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 336)
AUTHORS NCI CGAP
TITLE NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@nci.nih.gov
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 315.
Location/Qualifiers
1. 336
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1708830"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NBH19W"
/note="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAGTGGAGCGGCGGCGATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M. Fatima Bonaldo. This library was constructed from the
same fetuses as the fetal lung library, Soares fetal lung
NBH19W."

ORIGIN

Query Match 22.6%; Score 201; DB 1; Length 336;
Best Local Similarity 99.6%; Pred. No. 6.6e-94;
Matches 251; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

608 TGAACCGTAAGTGTGTTCTCAATATTTCCGTCCTCTGAGATCAATTAAGTC 667
285 TGAACCGTAAGTGTGTTCTCAATATTTCCGTCCTCTGAGATCAATTAAGTC 226

668 CTCACATCGCCGCTTTTCTCTGACAGCTTAAGCTTCTCTAAGCTTCCGCTCCAGG 727
225 CTCACATCGCCGCTTTTCTCTGACAGCTTAAGCTTCTCTAAGCTTCCGCTCCAGG 166

728 CCTGGGCCCACTTACCTTCCACCGGCTTCTGCGCGGAGTGGTGGGCAAGGCT 787
165 CCTGGGCCCACTTACCTTCCACCGGCTTCTGCGCGGAGTGGTGGGCAAGGCT 106

788 ATGTACTGTGTTCCCTTGTGACACTGGTGGCGGCGGAGAACTATCAATTAAGCC 847
105 ATGTACTGTGTTCCCTTGTGACACTGGTGGCGGCGGAGAACTATCAATTAAGCC 46

848 TGTCTGTTCCAT 859
45 TGTCTGTTCCAT 34

RESULT 3
A0357151/c 243 bp DNA linear GSS 24-JAN-1999
LOCUS A0357151
DEFINITION CITBI-EI-2534014.TF CITBI-EI Homo sapiens genomic clone 2534014,
genomic survey sequence.
ACCESSION A0357151
VERSION A0357151.1 GI:4184324
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 243)

AUTHORS
Zhao, S., Adams, M.D., Niernan, W., Malek, J., Shizuya, H., Simon, M. and Venter, J.C.
Use of BAC End Sequences from Caltech Libraries for Sequence-Ready Map Building
Unpublished (1997)
Other_GSSs: CTR1-El-2534014.TR
Contact: Shaying Zhao, William Niernan, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: bhe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES
source
1..243
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2534014"
/sex="male"
/cell_type="sperm"
/clone_lib="CTR1-El"
/note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"

ORIGIN
Query Match 19.5%; Score 174; DB 8; Length 243;
Best Local Similarity 100.0%; Pred. No. 1e-79;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 315 TGAACCGCTAGAAAGGATCTCTCTCAACCTCCCGGCTGACGACCTTGCGCGGAGG 374
DB 228 TGAACCGCTAGAAAGGATCTCTCTCAACCTCCCGGCTGACGACCTTGCGCGGAGG 169
QY 375 ACCCGACCCCGGAGAAACCCCTGCTCTGCTGCTGAGGTGAGCAACGACCTCAGGA 434
DB 168 ACCCGACCCCGGAGAAACCCCTGCTCTGCTGCTGAGGTGAGCAACGACCTCAGGA 109
QY 435 GAGCGCAGACTAGACCCGCGGAGAGTACAGATGAGTCCCTCAG 488
DB 108 GAGCGCAGACTAGACCCGCGGAGAGTACAGATGAGTCCCTCAG 55

RESULT 4
A0136453 372 bp DNA linear GSS 24-SEP-1998
LOCUS HS_3040_B2_F03_MF CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate=3040 Col=6 Row=L, genomic survey
sequence.
A0136453
VERSION A0136453.1 GI:3527789
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 372)
AUTHORS Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
JOURNAL 99380589
MEDLINE 10449764
PUBMED
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington

AUTHORS
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3040 row: L column: 6
Class: BAC ends
High quality sequence stop: 372.

FEATURES
source
1..372
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3040 Col=6 Row=L"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"

ORIGIN
Query Match 14.5%; Score 129; DB 8; Length 372;
Best Local Similarity 99.4%; Pred. No. 5e-56;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 684 TTTCCTGACAGGCTAGGCTACTCTCTACCTGCTCCAGGCTCGGCCCACTAC 743
DB 26 TTTCCTGACAGGCTAGGCTACTCTCTACCTGCTCCAGGCTCGGCCCACTAC 85
QY 744 CTCGCCCGGCTTCTCTGCGCGGCGATGCTGCGGCAAGGCTATGATGTTCC 803
DB 86 CTCGCCCGGCTTCTCTGCGCGGCGATGCTGCGGCAAGGCTATGATGTTCC 145
QY 804 TTTCGCCAGCTGCTGCGCGGCGGAGGAGTATATAGTACAGTGTCTTCATGAAA 863
DB 146 TTTCGCCAGCTGCTGCGCGGCGGAGGAGTATATAGTACAGTGTCTTCATGAAA 205

RESULT 5
AF057073/c 763 bp DNA linear GSS 21-FEB-2001
LOCUS AF057073 Human Homo sapiens genomic clone 3R probe, genomic survey
DEFINITION sequence.
AF057073
VERSION AF057073.1 GI:3142380
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 763)
AUTHORS Janer, M. and Geraghty, D.E.
The human major histocompatibility complex: 42,221 bp of genomic
sequence, high-density sequence-tagged site map, evolution, and
polymorphism for HLA class I
Genomics 51 (1), 35-44 (1998)
JOURNAL 98360090
MEDLINE 9693031
PUBMED
COMMENT Contact: Janer M
Geraghty Lab
Fred Hutchinson Cancer Research Center
1100 Fairview Ave., D2-100, Seattle, WA 98109-1024, USA
Email: geraghty@fhcrc.org
Class: unknown.
Location/Qualifiers
1..763
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="6p21.3; HLA Class I region"
/clone="3R probe"
/clone_lib="Human"

FEATURES
source
1..763
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="6p21.3; HLA Class I region"
/clone="3R probe"
/clone_lib="Human"

ORIGIN

Query Match 8.6%; Score 77; DB 8; Length 763;
 Best Local Similarity 100.0%; Pred. No. 1.2e-28;
 Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTTGGGGTCCAGGACCCAGACTCAGCCACCCAGCTTTGGGGGCCAGTACATA 60
 DB 155 CCTTTGGGGTCCAGGACCCAGACTCAGCCACCCAGCTTTGGGGGCCAGTACATA 96

QY 61 GCCATGATCCCACTG 77
 DB 95 GCCATGATCCCACTG 79

RESULT 6
 AA763309 332 bp mRNA linear EST 27-JAN-1998
 LOCUS vW91a02.r1 Stratiagene mouse skin (#937313) Mus musculus cDNA clone
 DEFINITION IMAGE:1229738 5', mRNA sequence.

ACCESSION AA763309 GI:2813056
 VERSION AA763309.1
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 332)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

EMAIL: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:655213
 Seq primer: -28ml3 rev1 ET from Amersham
 High quality sequence stop: 329.

FEATURES
 source
 1..332
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:1229621"
 /sex="females"
 /tissue_type="whole skin"
 /dev_stage="11 weeks old"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratiagene mouse skin (#937313)"
 /note="Organ: skin; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGACGACG 3' ~3' adaptor sequence: 5' CTCGAGTTT TTT TTT TTT TTT 3'."

ORIGIN
 Query Match 4.3%; Score 38; DB 1; Length 332;
 Best Local Similarity 100.0%; Pred. No. 3.6e-08;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 CCCAGCCCCCAGAAACCCCTGGGCTCTCTGCCCCCTGAG 414
 DB 215 CCCAGCCCCCAGAAACCCCTGGGCTCTCTGCCCCCTGAG 252

RESULT 7
 AA168568 361 bp mRNA linear EST 12-FEB-1997
 LOCUS m31c08.r1 Stratiagene mouse skin (#937313) Mus musculus cDNA clone
 DEFINITION IMAGE:608558 5', mRNA sequence.

ACCESSION AA168568 GI:1746771
 VERSION AA168568.1
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 361)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

EMAIL: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:373990
 Putative full length read
 vector to vector length is 515
 Seq primer: -28ml3 rev1 ET from Amersham
 High quality sequence stop: 352.

FEATURES
 source
 1..361
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:608558"
 /sex="females"
 /tissue_type="whole skin"
 /dev_stage="11 weeks old"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratiagene mouse skin (#937313)"
 /note="Organ: skin; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGACGACG 3' ~3' adaptor sequence: 5' CTCGAGTTT TTT TTT TTT TTT 3'."

ORIGIN
 Query Match 4.3%; Score 38; DB 1; Length 361;
 Best Local Similarity 100.0%; Pred. No. 3.7e-08;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 CCCAGCCCCCAGAAACCCCTGGGCTCTCTGCCCCCTGAG 414
 DB 23 CCCAGCCCCCAGAAACCCCTGGGCTCTCTGCCCCCTGAG 60

RESULT 8
 AA791103 379 bp mRNA linear EST 06-FEB-1998
 LOCUS vW91a02.r1 Stratiagene mouse skin (#937313) Mus musculus cDNA clone
 DEFINITION IMAGE:1229738 5', mRNA sequence.

ACCESSION AA791103 GI:2851223
 VERSION AA791103.1
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 379)
REFERENCE
AUTHORS Maira, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Maira M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:555330
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 360.
Location/Qualifiers
1. 379
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1229738"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse skin (#93713)"
/note="Organ: skin; Vector: plusdescript SK-; Site: 1; EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGACGACG 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'"

ORIGIN
Query Match 4.3%; Score 38; DB 1; Length 379;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 CCCAGCCCCCAGAAACCCCTGCGCTCTGCTGAG 414
DB 79 CCAGCCCCCAGAAACCCCTGCGCTCTGCTGAG 116

RESULT 9
CG481452 416 bp DNA linear GSS 01-OCT-2003
LOCUS OST13885 Mus musculus 1295v/Bv Mus musculus genomic clone OST13885,
DEFINITION genomic survey sequence.
ACCESSION CG481452
VERSION CG481452.1 GI:37233834
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 416)
REFERENCE
AUTHORS Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Pijgott, J., Beltrande-Rio, H., Buxton, E.C., Edwards, J., Finch, R.A., Fiddler, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jasing, C., Key, B.W., Jr., Kipp, P., Konhaufl, B., Ma, Z., -Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z., -Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, O., Person, C. and Sands, A.T.
TITLE Mx1 kinase deficiency lowers blood pressure in mice: a gene-trap

JOURNAL screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT Contact: Zambrowicz BP
Omnibank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene trap.
Location/Qualifiers
1. 416
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Bv"
/db_xref="taxon:10090"
/clone="OST13885"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Bv"

ORIGIN
Query Match 4.3%; Score 38; DB 9; Length 416;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 CCCAGCCCCCAGAAACCCCTGCGCTCTGCTGAG 414
DB 255 CCAGCCCCCAGAAACCCCTGCGCTCTGCTGAG 292

RESULT 10
A1596929 422 bp mRNA linear EST 21-APR-1999
LOCUS VJ4611.Y1 Stratagene mouse skin (#93713) Mus musculus cDNA clone
DEFINITION VJ4611.Y1 Stratagene mouse skin (#93713) Mus musculus cDNA clone
ACCESSION A1596929
VERSION A1596929.1 GI:4605977
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 422)
REFERENCE
AUTHORS Maira, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowles, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurr, R., Riter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
TITLE The WashU-NCI Mouse EST Project 1999
JOURNAL Unpublished (1999)
COMMENT Contact: Maira M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:537028
This read is a RESSEQUENCE of a previously sequenced mouse clone
correct orientation)
Seq primer: -40BP from Gibco
High quality sequence stop: 396.
Location/Qualifiers
1. 422
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:932108"
/sex="females"
/tissue_type="whole skin"

Query Match
 Best Local Similarity 100.0%; Score 38; DB 1; Length 422;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 /dev_stage="11 weeks old"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene mouse skin (#937313)"
 /note="Organ: skin; Vector: pBluescript SK-; Site 1:
 EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
 Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
 Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
 adaptor sequence: 5' GAATTCGACGAG 3' ~3' adaptor
 sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3'"

ORIGIN
 Query Match
 Best Local Similarity 100.0%; Score 38; DB 1; Length 422;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 377 CCCAGCCCCCAGAAAACCCCTGCTCTGCTGCTGAG 414
 282 CCCAGCCCCCAGAAAACCCCTGCTCTGCTGCTGAG 319

RESULT 11
 CG487403 442 bp DNA linear GSS 01-OCT-2003
 LOCUS OST22893 Mus musculus 129Sv/Ev Mus musculus genomic clone OST22893,
 DEFINITION genomic survey sequence.
 ACCESSION CG487403
 VERSION CG487403.1 GI:37246315
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 442)
 Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
 Piggott,J., BeltrandeRio,H., Buxton,B.C., Edwards,J., Finch,R.A.,
 Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaling,C.,
 Key,B.W., Jr., Klipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
 Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
 Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
 Zhu,Q., Person,C. and Sands,A.T.
 Mx1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 Contact: Zambrowicz BP
 OmniBank
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap.

FEATURES
 source
 Location/Qualifiers
 1..442
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST22893"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129Sv/Ev"

ORIGIN
 Query Match
 Best Local Similarity 100.0%; Score 38; DB 9; Length 442;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 377 CCCAGCCCCCAGAAAACCCCTGCTCTGCTGCTGAG 414
 239 CCCAGCCCCCAGAAAACCCCTGCTCTGCTGCTGAG 276

RESULT 12
 AA798896

LOCUS AA798896 451 bp mRNA linear EST 10-FEB-1998
 DEFINITION v994e08.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
 IMAGE:1230086 5', mRNA sequence.
 ACCESSION AA798896
 VERSION AA798896.1 GI:2861851
 KEYWORDS EST.
 SOURCE Mus musculus
 ORGANISM Mus musculus (house mouse)

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 451)
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Treister,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LIND, contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:655678

FEATURES
 source
 Location/Qualifiers
 1..451
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:1230086"
 /sex="females"
 /issue_type="whole skin"
 /dev_stage="11 weeks old"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene mouse skin (#937313)"
 /note="Organ: skin; Vector: pBluescript SK-; Site 1:
 EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
 Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
 Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
 adaptor sequence: 5' GAATTCGACGAG 3' ~3' adaptor
 sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3'"

ORIGIN
 Query Match
 Best Local Similarity 100.0%; Score 38; DB 1; Length 451;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 377 CCCAGCCCCCAGAAAACCCCTGCTCTGCTGCTGAG 414
 177 CCCAGCCCCCAGAAAACCCCTGCTCTGCTGCTGAG 214

RESULT 13
 CG484009 451 bp DNA linear GSS 01-OCT-2003
 LOCUS OST17807 Mus musculus 129Sv/Ev Mus musculus genomic clone OST17807,
 DEFINITION genomic survey sequence.
 ACCESSION CG484009
 VERSION CG484009.1 GI:37239343
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 451)
 AUTHORS Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
 Piggett,J., Beltrande,Rio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
 Fridde,C.J., Gupta,A., Hansen,G., Hu,X., Huang,C.,
 Kay,B.W., Jr., Kipp,P., Konhauft,B., Ma,Z., Markesich,D.,
 Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.,
 Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
 Zhu,Q., Person,C. and Sands,A.T.
 Wnt1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 COMMENT Contact: Zambrowicz BP
 OmniBank
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap.

FEATURES
 source Location/Qualifiers
 1..451
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST17807"
 /cell_type="embryonic stem cell"
 /clone_id="Mus musculus 129Sv/Ev"

ORIGIN
 Query Match 4.3%; Score 38; DB 9; Length 451;
 Best Local Similarity 100.0%; Pred. No. 3.7e-08;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 CCCAGCCCCCAGAAACCCCTGCGCTCTCTGAG 414
 256 CCCAGCCCCCAGAAACCCCTGCGCTCTGAG 293

RESULT 14
 BH098389 489 bp DNA linear GSS 19-JUL-2001
 LOCUS RPCI-24-372N23.TV RPCI-24 Mus musculus genomic clone
 DEFINITION RPCI-24-372N23, genomic survey sequence.
 ACCESSION BH098389
 VERSION BH098389.1 GI:14920132
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 489)
 Zhao,S., Nierman,W., Malek,J., Shatman,S., Akintec,B., Levin,M.,
 Tegayev,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregorgis,E.,
 Russell,D., de Jong,P. and Fraser,C.M.
 Mouse BAC End Sequences from Library RPCI-24
 Unpublished (1993)
 TITLE Contact: Shaying Zhao
 JOURNAL Department of Eukaryotic Genomics
 COMMENT The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-24. For BAC
 library availability, please contact Pieter de Jong
 (pdejong@mail.cho.org). Clones may be purchased from BACPAC
 Resources (http://www.choi.org/bacpac/orderframe.html). BAC end
 page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 372 Row: N Column: 23
 Seq primer: T7
 Class: BAC ends.
 Location/Qualifiers

source 1..489
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-24-372N23"
 /sex="Male"
 /cell_type="Spleen/Brain"
 /clone_id="RPCI-24"
 /note="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI;
 RPCI-24 Mouse BAC library produced by Pieter de Jong. The
 library was cloned in the pTARBAC1 cloning vector at the
 BamHI sites using MboI partially digested male C57BL/6J
 DNA."

ORIGIN
 Query Match 4.3%; Score 38; DB 8; Length 489;
 Best Local Similarity 100.0%; Pred. No. 3.7e-08;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 CCCAGCCCCCAGAAACCCCTGCGCTCTCTGAG 414
 447 CCCAGCCCCCAGAAACCCCTGCGCTCTCTGAG 410

RESULT 15
 AA530301 562 bp mRNA linear EST 22-JUL-1997
 LOCUS VJ46el1.r1 Stragene mouse skin (#937313) Mus musculus cDNA clone
 DEFINITION IMAGE:932108 5', mRNA sequence.
 ACCESSION AA530301
 VERSION AA530301.1 GI:2273007
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 562)
 Geisel,S., Kucaba,T., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Scheilenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterson,R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 TITLE Contact: Marra M/Mouse EST Project
 JOURNAL WashU-HMI Mouse EST Project
 COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:537028
 Seq primer: -28ml3 rev1 ET from Amersham
 High quality sequence stop: 221.
 Location/Qualifiers
 1..562
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:932108"
 /sex="female"
 /tissue_type="whole skin"
 /dev_stage="11 weeks old"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_id="Stragene mouse skin (#937313)"
 /note="Organ: skin; Vector: pBluescript SK-; Site 1:
 BcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
 Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
 Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'

adaptor sequence: 5' GAATTCGACGAG 3' ~3' adaptor
 sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' "

Query Match 4.3%; Score 38; DB 1; Length 562;
 Best local Similarity 100.0%; Pred. No. 3.7e-08;
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 377 CCCAGCCCCCAGAAACCCCTGGCCTCCTGCCCTGAG 414
 |||||
 Db 281 CCCAGCCCCCAGAAACCCCTGGCCTCCTGCCCTGAG 318

Search completed: January 11, 2005, 11:38:28
 Job time : 3420 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_p2n model

Run on: January 11, 2005, 11:38:33 ; Search time 82.688 Seconds
(without alignments)
1169.061 Million cell updates/sec

Title: US-09-994-365-2
Perfect score: 808
Sequence: 1 MIMNKLILGILVLCILTRGI.....EVDNRPOEBPDLPPREYR 136

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+p2n.model -DB=x1h
-Q=/cgn2_1/USFTO.spool_h/US09994365/runat_10012005_172233_6845/app.query.fasta_1.590
-DB=Issued Patents NA -OPMT=faetap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -IOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosun62 -TRANS=human40.cdt
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USBR=US09994365 @CNC 1.1.93 @runat_10012005_172233_6845 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WANT_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA.*
1: /cgn2_6/prodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/prodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/prodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/prodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/prodata/1/ina/PCTUS.COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	304.5	37.7	248	4	US-09-621-976-9776
C 2	198.5	24.6	4403765	3	US-09-103-840A-2
C 3	198.5	24.6	4411529	3	US-09-103-840A-1
C 4	190.5	23.6	1926	2	US-09-249-585A-4
C 5	190.5	23.6	1931	2	US-09-130-114-2
C 6	188.5	23.3	4403765	3	US-09-103-840A-2
C 7	188.5	23.3	4411529	3	US-09-103-840A-1
C 8	182	22.5	114793	4	US-10-148-806-3
C 9	181	22.4	6530	2	US-08-146-930-1
C 10	181	22.4	6530	2	US-08-458-240-1
C 11	181	22.4	6530	5	PCT-US93-03993-1
C 12	180.5	22.3	1854	4	US-09-894-844-103

C 13	180	22.3	1280	3	US-09-060-756-4	Sequence 4, Appli
C 14	180	22.3	1280	4	US-09-670-314-4	Sequence 4, Appli
C 15	179.5	22.2	152331	3	US-09-128-155-16	Sequence 16, Appli
C 16	176	21.8	320	3	US-09-165-264-7	Sequence 7, Appli
C 17	176	21.8	320	3	US-09-165-264-14	Sequence 14, Appli
C 18	175	21.7	320	3	US-09-165-264-13	Sequence 13, Appli
C 19	174.5	21.6	2830	2	US-09-010-9288-1	Sequence 1, Appli
C 20	172.5	21.3	318	3	US-09-165-264-12	Sequence 12, Appli
C 21	172	21.3	320	3	US-09-165-264-11	Sequence 11, Appli
C 22	171.5	21.2	1173	4	US-09-894-844-60	Sequence 60, Appli
C 23	171	21.2	319	3	US-09-165-264-8	Sequence 8, Appli
C 24	171	21.2	1926	4	US-09-249-585A-2	Sequence 2, Appli
C 25	171	21.2	1926	4	US-09-410-399-3	Sequence 3, Appli
C 26	171	21.2	2580	3	US-09-050-863-2	Sequence 2, Appli
C 27	171	21.2	2580	3	US-09-359-081-2	Sequence 2, Appli
C 28	171	21.2	5452	2	US-09-130-114-1	Sequence 1, Appli
C 29	171	21.2	8705	4	US-09-647-344A-14	Sequence 14, Appli
C 30	171	21.2	9600	3	US-08-910-647-1	Sequence 1, Appli
C 31	171	21.2	9600	4	US-09-620-925-1	Sequence 1, Appli
C 32	171	21.2	10596	1	US-07-884-811-15	Sequence 15, Appli
C 33	171	21.2	10596	1	US-07-885-871-15	Sequence 15, Appli
C 34	171	21.2	10596	1	US-08-087-783A-15	Sequence 15, Appli
C 35	171	21.2	10596	1	US-08-194-088B-15	Sequence 15, Appli
C 36	171	21.2	10596	2	US-08-194-087-15	Sequence 15, Appli
C 37	171	21.2	10596	5	PCT-US93-04648-15	Sequence 15, Appli
C 38	171	21.2	16080	4	US-09-724-566A-48	Sequence 48, Appli
C 39	169	20.9	290	3	US-08-818-112-37	Sequence 37, Appli
C 40	169	20.9	290	3	US-08-818-111-37	Sequence 37, Appli
C 41	169	20.9	290	3	US-09-056-556-37	Sequence 37, Appli
C 42	169	20.9	290	4	US-09-072-596-37	Sequence 37, Appli
C 43	169	20.9	290	4	US-09-072-967-37	Sequence 37, Appli
C 44	168.5	20.9	1548	2	US-08-762-106-5	Sequence 5, Appli
C 45	168.5	20.9	1548	3	US-09-320-774-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-621-976-9776/C
Sequence 9776, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J. B.
APPLICANT: Jobert, S. Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 9776
LENGTH: 248
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 188
OTHER INFORMATION: n=a, g, c or t
US-09-621-976-9776

Alignment Scores:

Pred. No.: 8.74e-14
Score: 304.50
Percent Similarity: 88.33%
Best Local Similarity: 86.67%
Query Match: 37.69%
DB: 4
Gaps: 1

US-09-994-365-2 (1-136) x US-09-621-976-9776 (1-248)

Qy 78 G|U|T|H|G|V|A|L|T|P|P|R|O|G|I|U|P|R|O|C|A|T|H|A|S|P|R|O|G|I|N|P|R|O|C|A|T|G|P|R|O|
|||||

```
Db      184 GAAACTGAGCTCTGGCCCCCTGAACCGCTAGAACGATCTCTCAACCTCCCGGCT 125
Qy      98 AspAspProTrrpProAlagIyProGlnProGlu--AsnProTrrpProAlaPro 116
        |||::|||
Db      124 GACGACCTTGCGCGGAGAGACCCCGCCAGCCCCCAGAAACCCCTTGTSCCT 65
Qy      117 GluValAspAsnArgProGlnGluProAspLeuAspProAlaGlnGluTyrArg 136
        |||
Db      64 GAGGTGACACACGACCTCAGAGAGAGCCAGACCTAGACCCCGGGAAGATACAGA 5

RESULT 2
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 11, 2005, 11:50:49 : Search time 489.056 Seconds
(without alignments)
1595.608 Million cell updates/sec

Title: US-09-994-365-2
Perfect score: 808
Sequence: 1 MILNWLGLGLVLCIHTRG1.....EVDNRQBPEDDLPPEBYR 136

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4293498 segs, 2868903791 residues
Total number of hits satisfying chosen parameters: 8586996

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ .p2n.model -DEV=X1h
-Q=cgnt2_1/USPTO.spool.h/US09994365/runat_10012005.172233.6861/app.query.fasta_1.590
-DB=Published Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blosum62
-TRANS=humano.ccl -LIST=45 -DOCALLIGN=200 -THR SCORE=oct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=frame -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09994365 @CGN_1.1.582 @runat_10012005.172233.6861
-NCPU=6 -ICPU=3 -NO MMAR -LARGQUEURY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-Fgapop=6 -Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -Delop=6 -Delext=7

Database :

Published Applications_NA: *
1: /cgnt2_6/ptodata/2/pubpna/US07_PUBCOMB.seq: *
2: /cgnt2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq: *
3: /cgnt2_6/ptodata/2/pubpna/US06_NEW_PUB.seq: *
4: /cgnt2_6/ptodata/2/pubpna/US06_PUBCOMB.seq: *
5: /cgnt2_6/ptodata/2/pubpna/US07_NEW_PUB.seq: *
6: /cgnt2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq: *
7: /cgnt2_6/ptodata/2/pubpna/US08_NEW_PUB.seq: *
8: /cgnt2_6/ptodata/2/pubpna/US08_PUBCOMB.seq: *
9: /cgnt2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq: *
10: /cgnt2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq: *
11: /cgnt2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq: *
12: /cgnt2_6/ptodata/2/pubpna/US09_NEW_PUB.seq: *
13: /cgnt2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq: *
14: /cgnt2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq: *
15: /cgnt2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq: *
16: /cgnt2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq: *
17: /cgnt2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq: *
18: /cgnt2_6/ptodata/2/pubpna/US10F_NEW_PUB.seq: *
19: /cgnt2_6/ptodata/2/pubpna/US11_NEW_PUB.seq: *
20: /cgnt2_6/ptodata/2/pubpna/US60_NEW_PUB.seq: *
21: /cgnt2_6/ptodata/2/pubpna/US60_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

*

Result No.	Score	Query Match	Length	DB ID	Description
1	808	100.0	891	9 US-09-994-365-1	Sequence 1, Appl
2	712	88.1	2997	9 US-09-994-365-10	Sequence 10, Appl
3	712	88.1	3001	9 US-09-994-365-4	Sequence 4, Appl
4	712	88.1	25235	17 US-10-164-230-2	Sequence 2, Appl
5	712	88.1	55050	17 US-10-467-752-4	Sequence 4, Appl
6	486	60.1	565	15 US-10-029-386-5700	Sequence 5700, Ap
7	449	55.6	3673778	15 US-10-312-841-1	Sequence 1, Appl
8	314	38.9	157	15 US-10-029-386-19510	Sequence 19510, Ap
9	199	24.6	711	16 US-10-282-122A-31860	Sequence 31860, A
10	198.5	24.6	2772	16 US-10-282-122A-28290	Sequence 28290, A
11	197	24.4	573	17 US-10-767-701-4301	Sequence 4301, Ap
12	196	24.3	766	18 US-10-425-115-82176	Sequence 82176, A
13	195.5	24.2	446	9 US-09-864-761-20699	Sequence 20699, A
14	195	24.1	12733	14 US-10-032-393-47	Sequence 47, Appl
15	195	24.1	12739	14 US-10-032-393-8	Sequence 8, Appl
16	193	23.9	985	18 US-10-425-115-91623	Sequence 91623, A
17	191	23.6	426	17 US-10-021-323-5998	Sequence 5998, Ap
18	190	23.5	916	18 US-10-425-115-47293	Sequence 47293, A
19	189.5	23.5	815	16 US-10-424-599-20495	Sequence 20495, A
20	189	23.4	925	17 US-10-437-963-44536	Sequence 44536, A
21	188.5	23.3	600	18 US-10-363-345A-39087	Sequence 39087, A
22	188.5	23.3	600	18 US-10-363-345A-39088	Sequence 39088, A
23	188	23.3	545	17 US-10-437-963-56258	Sequence 56258, A
24	188	23.3	1493	15 US-10-029-386-25133	Sequence 25133, A
25	187.5	23.2	1327	16 US-10-398-221-1265	Sequence 1265, Ap
26	186.5	23.1	629	17 US-10-021-323-9375	Sequence 9375, Ap
27	186.5	23.1	821	18 US-10-425-115-131043	Sequence 131043, A
28	186	23.0	700	18 US-10-425-115-14077	Sequence 14077, A
29	186	23.0	1455	16 US-10-282-122A-28683	Sequence 28683, A
30	185.5	23.0	1245	17 US-10-021-323-9377	Sequence 9377, Ap
31	185.5	23.0	1245	17 US-10-437-963-94850	Sequence 94850, A
32	185.5	23.0	1744	17 US-10-437-963-19774	Sequence 19774, A
33	184.5	22.8	485	16 US-10-424-599-65670	Sequence 65670, A
34	184	22.8	882	17 US-10-437-963-28390	Sequence 28390, A
35	183.5	22.7	3163	15 US-10-017-161-1857	Sequence 1857, Ap
36	183.5	22.7	3163	15 US-10-292-798-1513	Sequence 1513, Ap
37	183	22.6	590	18 US-10-425-115-13328	Sequence 13328, A
38	182.5	22.6	415	17 US-10-021-323-12908	Sequence 12908, A
39	182.5	22.6	659	17 US-10-767-701-4135	Sequence 4135, Ap
40	182.5	22.6	823	18 US-10-425-115-53676	Sequence 53676, A
41	182.5	22.6	965	15 US-10-029-386-22737	Sequence 22737, A
42	182.5	22.6	1083	15 US-10-029-386-20723	Sequence 20723, A
43	182.5	22.6	2862	9 US-09-888-615-7	Sequence 7, Appl
44	182.5	22.6	3067	16 US-10-311-035-42	Sequence 42, Appl
45	182	22.5	497	16 US-10-424-599-133788	Sequence 133788, A

ALIGNMENTS

RESULT 1
US-09-994-365-1
Sequence 1, Application US/09994365
Patent No. US20020115148A1
GENERAL INFORMATION:
APPLICANT: Charmsley, Patrick
APPLICANT: Mosen, Patrick
APPLICANT: Mosen, Patrick
TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
FILE REFERENCE: CECH118109
CURRENT APPLICATION NUMBER: US/09/994,365
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: US 60/253,592
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/256,839
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 891
TYPE: DNA

```
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (64)..(471)
US-09-994-365-1

Alignment Scores:
Pred. No.: 6,33e-61      Length: 891
Score: 808.00           Matches: 136
Percent Similarity: 100.00%  Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00%      Gaps: 0
DB: 9

US-09-994-365-2 (1-136) x US-09-994-365-1 (1-891)

Qy 1 MetlleuAentPlyleuLeuGlyYleuValleuCyseuH1stHrArgGlyYle 20
Db 64 ATGATCTCTCAAGCTCTGAGATCTGATCTGCTTGTCTGCAACCAAGGATC 123
Qy 21 SerGlySerGlyYH1SProSerH1SProProAlaGluAspArgGluGluAlaGlySer 40
Db 124 TCAGGACGAGGCGCCACCTCTCAACCCGACAGACGAGAGGAGGAGGCTCC 183
Qy 41 ProThrLeuProGlnGlyProProValProGlyAspProTTPProGlyAlaProProLeu 60
Db 184 CCAACATGCTCTCAAGGCGCCCGCAGTCCCGGTGACCTTGCCAGGAGGACCCCTCTC 243
Qy 61 PheGluAspProProProThraArgProSerArgProTTPArgAspLeuProGluThrGly 80
Db 244 TTGAAATCTCTCGCTTACCGCCGACGTCGTCTCGAGAGACCTGCTGAAACTGGA 303
Qy 81 ValTTPProProGluProProArgThraSPProProGlnProProAlaProAspAspPro 100
Db 304 GTCTGCGCCCTGAAACCGCTAGAACGATCTCTCACTCCCGGCTGAGACCT 363
Qy 101 TTPProAlaGlyProGlnProProGluAspProTTPProProAlaProGluAlaAspAsn 120
Db 364 TGGCGGACAGAGACCCGACCCGACGAAACCCCTGCTCTGAGGTGACCAAC 423
Qy 121 ArgProGlnGluGluProAspAspLeuAspProProArgGluGluTyrArg 136
Db 424 CGACCTCAGAGAGAGCCAGACTTGAACCCCGGAGAGATGACAGA 471

RESULT 2
US-09-994-365-10
/ Sequence 10, Application US/09994365
/ Patent No. US20020115148A1
/ GENERAL INFORMATION:
/ APPLICANT: Charmley, Patrick
/ APPLICANT: Moss, Patrick
/ APPLICANT: McEuen, Mark
/ TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
/ FILE REFERENCE: CECH18109
/ CURRENT APPLICATION NUMBER: US/09/994,365
/ PRIOR FILING DATE: 2001-11-26
/ PRIOR APPLICATION NUMBER: US 60/253,592
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US 60/256,839
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 10
/ LENGTH: 2997
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-994-365-10

Alignment Scores:
Pred. No.: 3.15e-52      Length: 2997
Score: 712.00           Matches: 118
Percent Similarity: 100.00%  Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00%      Gaps: 0
```

```
Query Match: 88.12%      Indels: 0
DB: 9      Gaps: 0

US-09-994-365-2 (1-136) x US-09-994-365-10 (1-2997)

Qy 19 GlyYleSerGlySerGlyYH1SProSerH1SProProAlaGluAspArgGluGluAla 38
Db 2201 GGATCTCAAGGACGAGGCGCCACCTCTCAACCCGACAGACGAGAGGAGGCA 2260
Qy 39 GlySerProThrLeuProGlnGlyProProValProGlyAspProTTPProGlyAlaPro 58
Db 2261 GGCTCCCAACATGCTCTCAAGGCGCCCGCAGTCCCGGTGACCTTGCCAGGAGGACCC 2320
Qy 59 ProLeuPheGluAspProProProThraArgProSerArgProTTPArgAspLeuProGlu 78
Db 2321 CTTCTTGAATCTCTCGCTTACCGCCGACGTCGTCTCGAGAGACTGCTTGA 2380
Qy 79 ThrGlyValTTPProProGluProProArgThraSPProProGlnProProAlaProAsp 98
Db 2381 ACTGAGTCTGCGCCCTGAAACCGCTAGAACGATCTCTCACTCCCGGCTGAC 2440
Qy 99 AspProTTPProAlaGlyProGlnProProGluAspProTTPProProAlaProGluAla 118
Db 2441 GACCTTGGCGGACAGAGACCCGACCCGACGAAACCCCTGCTCTGCTGAGGTG 2500
Qy 119 AspAsnArgProGlnGluGluProAspAspLeuAspProProArgGluGluTyrArg 136
Db 2501 GACACCGACTCTCAGAGAGAGCCAGACTTGAACCCCGGAGAGATGACAGA 2554

RESULT 3
US-09-994-365-4
/ Sequence 4, Application US/09994365
/ Patent No. US20020115148A1
/ GENERAL INFORMATION:
/ APPLICANT: Charmley, Patrick
/ APPLICANT: Moss, Patrick
/ APPLICANT: McEuen, Mark
/ TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
/ FILE REFERENCE: CECH18109
/ CURRENT APPLICATION NUMBER: US/09/994,365
/ PRIOR FILING DATE: 2001-11-26
/ PRIOR APPLICATION NUMBER: US 60/253,592
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US 60/256,839
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4
/ LENGTH: 3001
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-994-365-4

Alignment Scores:
Pred. No.: 3.16e-52      Length: 3001
Score: 712.00           Matches: 118
Percent Similarity: 100.00%  Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 88.12%      Gaps: 0
DB: 9

US-09-994-365-2 (1-136) x US-09-994-365-4 (1-3001)

Qy 19 GlyYleSerGlySerGlyYH1SProSerH1SProProAlaGluAspArgGluGluAla 38
Db 2205 GGATCTCAAGGACGAGGCGCCACCTCTCTCAACCCGACAGAGACGAGAGGCA 2264
Qy 39 GlySerProThrLeuProGlnGlyProProValProGlyAspProTTPProGlyAlaPro 58
Db 2265 GGCTCCCAACATGCTCTCAAGGCGCCCGCAGTCCCGGTGACCTTGCCAGGAGGCA 2324
Qy 59 ProLeuPheGluAspProProProThraArgProSerArgProTTPArgAspLeuProGlu 78
```

Db 2325 CCTCTCTTTGAAATCTCCGCTACCCGCGGAGAGACCTGCTGAA 2384
Qy 79 ThrGlyValTrpProGluProProArgThrAspProProGluProProArgProAsp 98
Db 2385 ACTGGATCTGGCCCCCTGAACCGCTTAGAACGATCTCTCAACTCTCCCGGCTGAC 2444
Qy 99 AspProTrpProAlaGlyProGluProProGluAsnProTrpProProAlaProGluVal 118
Db 2445 GACCTTGCGCGGAGAGACCCGAGAAAACCTTGCTGCTGCGCTGAGGTG 2504
Qy 119 AspAsnArgProGluGluGluProAspLeuAspProProAlaGluGluTrpArg 136
Db 2505 GACAACCGACTCAGAGAGAGCCAGACTTAGACCCCGGAAAGTACAGA 2558

RESULT 4
US-10-164-230-2
; Sequence 2, Application US/10164230
; Publication No. US20030170652A1
; GENERAL INFORMATION:
; APPLICANT: Inoko, Hidetoshi
; APPLICANT: Tamiya, Gen
; TITLE OF INVENTION: METHOD OF TESTING FOR PSORIASIS VULGARIS
; FILE REFERENCE: 06501-112U51
; CURRENT APPLICATION NUMBER: US/10/164,230
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: PCT/JP00/08624
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: JP 11/346867
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 25235
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1) ... (420)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1282) ... (1405)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1602) ... (1702)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1602) ... (1631)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (2352) ... (2364)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (6287) ... (6509)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (10417) ... (10493)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (14244) ... (14407)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (14244) ... (14344)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (25190) ... (25235)
; US-10-164-230-2

Alignment Scores:
Pred. No.: 1,85e-51 Length: 25235
Score: 712.00 Matches: 118
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.12% Indels: 0

DB: 15 Gaps: 0
US-09-994-365-2 (1-136) x US-10-164-230-2 (1-25235)
Qy 19 GlyIleSerGlySerGluGlyHisProSerHisProProAlaGluAspArgGluVal 38
Db 1754 GGCATTCACAGCGAGCGAGGCGCACCCCTTCACACCCGAGAGAGCCGAGAGAGCA 1813
Qy 39 GlySerProThrLeuProGluGluProProValProGlyAspProTrpProGlyValPro 58
Db 1814 GGTCCCAACATTGCTCAGAGGCGCCCGAGTCCCGGTAGCCTTGCGCAGGGGCAACC 1873
Qy 59 ProLeuPheGluAspProProProThrArgProSerArgProTrpArgAspLeuProGlu 78
Db 1874 CCTCTCTTTGAAATCTCCGCTACCCGCGGAGAGACCTGCTGCTGAGAGACCTGCTGAA 1933
Qy 79 ThrGlyValTrpProProGluProProArgThrAspProProGluProProArgProAsp 98
Db 1934 ACTGGATCTGGCCCCCTGAACCGCTTAGAACGATCTCTCAACTCTCCCGGCTGAC 1993
Qy 99 AspProTrpProAlaGlyProGluProProGluAsnProTrpProProAlaProGluVal 118
Db 1994 GACCTTGCGCGGAGAGACCCGAGAAAACCTTGCTGCTGCGCTGAGGTG 2053
Qy 119 AspAsnArgProGluGluGluProAspLeuAspProProAlaGluGluTrpArg 136
Db 2054 GACAACCGACTCAGAGAGAGCCAGACTTAGACCCCGGAAAGTACAGA 2107

RESULT 5
US-10-467-752-4
; Sequence 4, Application US/10467752
; Publication No. US20040161759A1
; GENERAL INFORMATION:
; APPLICANT: Lench, et al.
; TITLE OF INVENTION: Test and Model for Inflammatory disease
; FILE REFERENCE: 2003682-0009
; CURRENT APPLICATION NUMBER: US/10/467,752
; CURRENT FILING DATE: 2003-08-13
; PRIOR APPLICATION NUMBER: PCT/GB02/00653
; PRIOR FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: GB0103514.6
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 55050
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13351) ... (13351)
; OTHER INFORMATION: n is a o r t o r g o r c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13401) ... (13401)
; OTHER INFORMATION: n is a o r t o r g o r c
; US-10-467-752-4

Alignment Scores:
Pred. No.: 3.54e-51 Length: 55050
Score: 712.00 Matches: 118
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.12% Indels: 0
DB: 17 Gaps: 0

US-09-994-365-2 (1-136) x US-10-467-752-4 (1-55050)
Qy 19 GlyIleSerGlySerGluGlyHisProSerHisProProAlaGluAspArgGluVal 38
Db 2709 GGCATTCACAGCGAGCGAGGCGCACCCCTTCACACCCGAGAGAGCCGAGAGAGCA 27158
Qy 39 GlySerProThrLeuProGluGluProProValProGlyAspProTrpProGlyValPro 58

```

Db      27159  GGCTCCCCAACATGCTCCAGGGCCCCCAGTCCCGGTGACCTTGCCAGGGGACCC 27218
Qy      59      ProleuphegluaspProProProThArProseArProProTpaAgaApleuProGlu 78
Db      27219  CCTCTCTTTGAAGATCCTCGCCCTAACCCGCCAGTGTCTCTGGAAGACCTGCTGAA 27278
Qy      79      ThrglyValTrpProProGluProProArGThAsPProProGlnProProArGProAsp 98
Db      27279  ACTGGAAGTCTGGCCCCCTGAACCGCTAGAACGATCTCTCAACTCCCGGCTGAC 27338
Qy      99      AspProTrpProAlaGlyProGlnProProGluAsnProTrpProAlaProGluVal 118
Db      27339  GACCCCTGGCCGGCAGAGACCCCAACCCCAAAAAACCCCTGCTGCTGCTGAGAGTGT 27398
Qy      119     AspAsnArProGlnGluGluProAspLeuAspProProArGgGluGluTrpArg 136
Db      27399  GACAACCGACCTCAGGAGAGCCAGACCTAGACCACCCCGGAGAGTACAGA 27452

```

RESULT 6

```

US-10-029-386-5700
; Sequence 5700, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEWICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 5700
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB023060.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.82
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.82
; OTHER INFORMATION: SWISSPROT HIT: Q99715, EVALU6 6.20e-01
; OTHER INFORMATION: EST HUMAN HIT: BF513178.1, EVALU6 0.00e+00
; OTHER INFORMATION: NT HIT: g115304354, EVALU6 0.00e+00
US-10-029-386-5700

```

Alignment Scores:

```

Pred. No.: 2,2e-33 Length: 565
Score: 486.00 Matches: 79
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.15% Indels: 0
DB: 15 Gaps: 0

```

US-09-994-365-2 (1-136) x US-10-029-386-5700 (1-565)

```

Qy      58      ProProleuphegluaspProProProThArProseArProProTpaAgaApleuPro 77
Db      1      CCCCCCTCTTTGAAGATCCTCGCCCTAACCCGCCCAAGTGTCTCTGGAAGACCTGCT 60
Qy      78      GluThrGlyValTrpProProGluProProArGThAsPProProGlnProProArGPro 97
Db      61      GAAACTGAGTCTGGCCCCCTGAACCGCTAGAACGATCTCTCAACTCCCGGCT 120
Qy      98      AspAspProTrpProAlaGlyProGlnProProGluAsnProTrpProAlaProGlu 117
Db      121     GACGACCCCTTGGCCGGAGAGACCCCAAGCCCAAAAAACCCCTGCTGCTGCTGAG 180
Qy      118     ValAspAsnArProGlnGluGluProAspLeuAspProProArGgGluGluTrpArg 136
Db      181     GTGGACAACGACCTCAGAGAGCCAGACCTAGACCCACCCCGGAGAGTACAGA 237

```

RESULT 7

```

US-10-312-841-1/c
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: B01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 11, 2005, 09:34:16 ; Search time 362.064 Seconds
(without alignments)
1652.840 Million cell updates/sec

Title: US-09-994-365-3

Perfect score: 692

Sequence: 1 SEGHPHPADREDEAGSPF.....EVDNRPEBPDLPPEEYR 114

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODBL=frame+.p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/h/US0994365/runat_10012005_172231_6815/app.query.fasta_1.590
-DB=N.GeneSeq_23Sep04 -Qfmt=faa1cap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=p2n -NDBM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USBR=US0994365.QCGN_1.1.586 -runat_10012005_172231_6815 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEDQUERY -NRG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: N_GeneSeq_23Sep04:*

1: geneseqn1980s:*\n2: geneseqn1990s:*\n3: geneseqn2000s:*\n4: geneseqn2001as:*\n5: geneseqn2001bs:*\n6: geneseqn2002as:*\n7: geneseqn2002bs:*\n8: geneseqn2003as:*\n9: geneseqn2003bs:*\n10: geneseqn2003cs:*\n11: geneseqn2003ds:*\n12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	692	100.0	891	6	ABK86962 Human can
2	692	100.0	1473	6	ABN60006 Novel hum
3	692	100.0	2997	6	ABK86967 Human CAN
4	692	100.0	3001	6	ABK86963 Human can
5	692	100.0	25235	4	AAH45310 Human SEE
6	692	100.0	55050	6	ABQ75680 Human SEE

7	486	70.2	565	12	ACH72505	Ach72505 Human gen
8	314	45.4	157	12	ACH86315	Ach86315 Human gen
9	199	28.8	711	8	ACA43990	Prokaryot
10	198.5	28.7	2772	8	ACA04020	Prokaryot
11	198.5	28.7	110000	4	AAI99682_10	Continuation (11 o
12	198.5	28.7	110000	4	AAI99683_10	Continuation (11 o
13	190.5	27.5	446	4	AAI23276	Probe #13
14	190.5	27.5	446	4	ABA66382	Human foe
15	190.5	27.5	446	4	AAI48596	Probe #17
16	190.5	27.5	446	4	ABA50433	Human bre
17	190.5	27.5	446	4	ABA35379	Probe #13
18	190.5	27.5	446	4	AAK42529	Human bon
19	190.5	27.5	446	4	AAK16757	Human bra
20	190.5	27.5	446	4	ABS42140	Human liv
21	190.5	27.5	446	5	AAI08921	Probe #89
22	190.5	27.5	446	6	ABS16574	Human gen
23	188.5	27.2	600	6	ABQ52497	Abq52497 Oligonuc
24	188.5	27.2	600	6	ABQ52496	Abq52496 Oligonuc
25	188.5	27.2	110000	4	AAI99682_09	Continuation (10 o
26	188.5	27.2	110000	4	AAI99682_27	Continuation (10 o
27	188.5	27.2	110000	4	AAI99682_28	Continuation (10 o
28	188.5	27.2	110000	4	AAI99682_09	Continuation (10 o
29	188.5	27.2	110000	4	AAI99683_27	Continuation (28 o
30	188.5	27.2	110000	4	AAI99683_27	Continuation (28 o
31	187.5	27.1	1327	6	ABQ68452	Ach91938 Human gen
32	187.5	27.1	3946	2	AAT93610	Myobacte
33	186	26.9	1452	8	ACR39367	Myobacte
34	186	26.9	1455	8	ACA40813	Prokaryot
35	186	26.9	12733	6	ABK98631	Vector ps
36	186	26.9	12733	6	ACD13882	L. lactis
37	186	26.9	12739	6	ABK98592	Vector ps
38	186	26.9	12739	6	ACD13843	Plasmid p
39	186	26.9	110000	4	AAI99683_37	Continuation (38 o
40	186	26.9	110000	4	AAI99683_37	Continuation (38 o
41	184	26.6	7720	3	AAAS3800	Genomic D
42	184	26.6	110000	4	AAI99683_11	Continuation (12 o
43	183.5	26.5	3163	10	ADCG7060	Human GPC
44	183	26.4	1833	4	ABL22159	Drosophila
45	183	26.4	110000	4	AAI99682_39	Continuation (40 o

ALIGNMENTS

RESULT 1	ABK86962	standard; cDNA; 891 BP.
ID	ABK86962	
AC	ABK86962	
XX	24-SEP-2002	(first entry)
DE	Human candidate coding sequence-1 (CAN-1) cDNA.	
XX	Human; antipositive; chromosome 6; candidate coding sequence-1; CAN-1;	
KW	SEK-1; STG; human leukocyte antigen C; HLA C; HLA Cw6; psoriasis; skin;	
KW	keratinocyte; chronic inflammatory dermatosis; erythroderma; seboreic;	
KW	gutrate; pustular variant; Reiter's disease; hyperproliferation;	
KW	epidermis; differentiation; diagnosis; gene therapy; gene; ss; SNP;	
XX	single nucleotide polymorphism.	
OS	Homo sapiens.	
XX		
Key	Location/Qualifiers	
FT	64..474	
FT	/*tag= a	
FT	/product= "CAN-1"	
FT	64..129	
FT	sig_peptide	
FT	/*tag= b	
FT	130..471	
FT	/*tag= c	
FT	/note= "Mature CAN-1"	
FT	variation	
FT	/*tag= d	

FT	/standard_name= "Single nucleotide polymorphism"
XX	
PN	WO00024375-A2.
XX	
PD	06-JUN-2002.
XX	
EF	27-NOV-2001, 2001WO-US044506.
XX	
PR	28-NOV-2000, 2000US-0253592P.
PR	15-DEC-2000, 2000US-0256839P.
XX	
PA	(CELL-) CELLTECH R & D INC.
XX	
PI	Charmley P, Moss P, McEuen M;
XX	
DR	WPI; 2002-508513/54.
DR	P-PSDB; AAU79579.
XX	
PT	Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation
PT	and differentiation, and polynucleotides encoding the polypeptide; useful
PT	for diagnosing or predicting susceptibility to psoriasis in individual.
XX	
PS	Claim 8; Page 80-81; 95pp; English.

Sequence 891 BP; 169 A; 339 C; 196 G; 187 T; 0 U; 0 Other;

Alignment Scores:	
Pred. No.:	2,96e-24
Score:	692.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	6
Gaps:	0
Length:	891
Matches:	114
Conservative:	0
Mismatches:	0
Indels:	0
	0

US-09-994-365-3 (1-114) X ABK86962 (1-891)

QY 1 SerCUGLYHisProSerHisProProAlaGluuAspArgGluGluAlaGlySerProThr 20
 |||||
 Db 130 AGCAGGGGCACCCCTCTCAACCCAGCAGACCGAGGAGGAGGAGGCTCCCAACA 189

QY 21 LeuProGlnGlyProProValProGlyAspProTrpProGlyAlaProProLeuPheGlu 40
 |||||
 Db 190 TTGCTCAGGGCCCCCAGTCCCGGTGACCTTGCCACAGGGGACCCCCCTCTTTGAA 249
 |||||

QY 41 AspProProProThrArgProSerArgProTrpArgAspLeuProGluThrGlyValTrp 60
 |||||
 250 GATCTCGGCTACCGCCAGTGTCTCCGGAAGACCTGCCTGAAACTGGAGTCTGG 309
 |||||

QY	61	ProProGluGluProProArgThrAspProProGluInpProArgProAspAspProTppPro	80
Db	310	CCCCCTGAACCGCCTTAGAACGGATCTCTCAACCTCCCGGCGCTGACGACACCTTGGCCG	369
QY	81	AlaGluProGluInpProProGluAspProTppProProAlaProGluValAspAsnArgPro	100
Db	370	GCAGGACCCCAACCCCCACGAAAAACCCCTGGCCTCTCTGCCCCCTGAGGTGGACACCGACCT	429
QY	101	GlnGlnGluProAspLeuAspProProArgGlnGluTyrArg	114
Db	430	CAGGAGAGCCAGACCTTAGACCCACCTCCCGGAGAGGTACAGA	471

RESULT 2
ABN60006
ID ABN60006 standard; cDNA; 1473 BP
yy

AC ABN60006;

DT 28-JUN-2002 (first entry)

DE Novel human coding sequence SEQ ID NO: 417.

KM Human; antihaemic; vulnery; antiinflammatory; immunomodulator;
KM antifertility; ceebropsective; cyostatic; rheumatic; gene therapy;
KM neuroprotective; antiapronsin; protein therapy; ESt;
KM expressed sequence tag; gene; ss.

OS Homo sapiens.

PN WO200222660-A2

PD 21-MAR-2002

PF 10-SEP-2001; 2001WO-US026015.

PR 11-SEP-2000; 2000US-00659671.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;

First XX XX

DR P-PSDB; ABB97593.

PT An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis.

PS Claim 1; SEQ ID NO 417; 509pp; English.

CC The present invention provides the protein and coding sequences of 444

(ESTs). They can be used to stimulate cell growth, to regulate

e.g. in burn treatment, to regulate the immune system e.g. to treat

CC infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke

CC rheumatoid arthritis, and to treat nervous system disorders e.g. multiple sclerosis.

CC invention

Sequence 1473 BP; 294 A; 491 C; 382 G; 306 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4,36e+24	147
Score:	632.00	114
Percent Similarity:	100.00%	
Best Local Similarity:	100.00%	
Query Match:	100.00%	
DB:	6	
	Gaps:	0

US-09-994-365-3 (1-114)	x	ABN60006 (1-1473)
Qy	1	SergIuGIyHlApProSeRiHlProProAlaGIuAsPaRgGIuGluAlaGIySeRProThr 20
Db	702	AGCGAGGGCCACCCCTCTCACCACCCGACAGACCGAGAGAGAGGCTGCCAACCA 761
Qy	21	LeuPProGIuNGIyProProValPProGIyAspProTrpProGIyAlaProProLeuPheGlu 40
Db	762	TTGCCCTGAGGGCCCCCAGCTCCCGGTACCCCTTGSCCAGGGGGACCCCTCTTTTAA 821
Qy	41	AspProProProThArGIyProSeRarPProTrPArGAsPleuProGIuThGIyValTrp 60
Db	822	GATCTCTCGGCTTACCCGCCCCAGTGTCTCTCTGAGAGACCTGCTGAAGTCTGAGTCTGG 881
Qy	61	ProProGIuPProProArGIyThAsPProProGIuProProArGIyProAspAspProTrpPro 80
Db	882	CCCCCTGAACCGCTTAGAACGGATCTCTCAACTCCCGGCTTGACGACCTTGCGCG 941
Qy	81	AlaGIyPProGIuPProProGIuAsnProTrpProProAlaProProGluValAspAsnArGIyPro 100
Db	942	GCAGGACCCCGACCCGCCAGAAACCCCTGGGCTCTGCGCCCTGAGGTGACACCGACT 1001
Qy	101	GIuGIuGIuPProAspPleuAspProProArGIuGIuGIyTrGIyArGIy 114
Db	1002	CAGGAGAGCCAGACTTAGACCCACCCCGGAGAGGTACAGA 1043
RESULT 3		
ID	ABK6967	standard; DNA; 2997 BP.
AC	ABK6967;	
XX	24-SEP-2002	(first entry)
DE	Human CAN-1 deletion polymorphism genomic DNA.	
XX	Human; antipneumatic; chromosome 6; candidate coding sequence-1; CAN-1;	
KM	SBEK-1; STG; human leukocyte antigen C; HLA C; HLA Cw6; psoriasis; skin;	
KW	keratinocyte; chronic inflammatory dermatosis; erythroderma; seborehnic;	
KV	gutrate; pustular variant; Reiter's disease; hyperproliferation;	
KW	epidermis; differentiation; diagnosis; gene therapy; gene; da; SNP;	
KM	single nucleotide polymorphism; deletion polymorphism.	
XX	Homo sapiens.	
OS		
XX	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	variation	replace(11..12,CCAGA)
FT		/*tag= a
FT		/note= "Deletion polymorphism"
FT	variation	replace(114,T)
FT		/*tag= b
FT		/standard name= "Single nucleotide polymorphism"
FT	variation	replace(361,A)
FT		/*tag= c
FT		/standard name= "Single nucleotide polymorphism"
FT	variation	replace(550,A)
FT		/*tag= d
FT		/standard name= "Single nucleotide polymorphism"
FT	variation	replace(966,G)
FT		/*tag= e
FT		/standard name= "Single nucleotide polymorphism"
FT	variation	replace(1096,T)
FT		/*tag= f
FT		/standard name= "Single nucleotide polymorphism"
FT	variation	replace(1196,A)
FT		/*tag= g
FT		/standard name= "Single nucleotide polymorphism"
FT	variation	replace(1390,T)
FT		/*tag= h
FT		/standard name= "Single nucleotide polymorphism"
FT	CDS	1481..2557
FT		/*tag= i
FT		/product= "CAN-1"

FT	exon	1481..1535	
FT		/*tag= j	
FT		/number=1	
FT	intron	1536..2201	
FT		/*tag= k	
FT		/number=1	
FT	variation	replace(1677,A)	
FT		/*tag= l	
FT		/standard_name=	"Single nucleotide polymorphism"
FT	variation	replace(1875,T)	
FT		/*tag= m	
FT		/standard_name=	"Single nucleotide polymorphism"
FT	variation	replace(1582,A)	
FT		/*tag= n	
FT		/standard_name=	"Single nucleotide polymorphism"
FT	variation	replace(2016,C)	
FT		/*tag= o	
FT		/standard_name=	"Single nucleotide polymorphism"
FT	variation	replace(2107,G)	
FT		/*tag= p	
FT	exon	/standard_name=	"Single nucleotide polymorphism"
FT		2202..2557	
FT		/*tag= q	
FT		/number=2	
FT	variation	replace(2393,T)	
FT		/*tag= r	
FT		/standard_name=	"Single nucleotide polymorphism"
FT	variation	replace(2651,G)	
FT		/*tag= s	
FT		/standard_name=	"Single nucleotide polymorphism"
FT	variation	replace(2618,G)	
FT		/*tag= t	
FT		/standard_name=	"Single nucleotide polymorphism"
FT	variation	replace(2871,C)	
FT		/*tag= u	
FT		/standard_name=	"Single nucleotide polymorphism"
PN	WO200244375-A2.		
PD	06-JUN-2002.		
XX			
XX	27-NOV-2001; 2001WO-US044506.		
PE			
XX			
XX	28-NOV-2000; 2000US-0253592P.		
PR	15-DEC-2000; 2000US-0256839P.		
XX			
PA	(CELL-) CELLTech R & D INC.		
P1			
P1	Charmley P, Moss P, Mceuen M;		
XX			
DR	WPI; 2002-508513/54.		
DR	P-PSDB; AAU79579.		
XX			
PS	Example 3; Page 92-93; 95pp; English.		
XX			
CC	The invention discloses isolated candidate coding sequence-1 (CAN-1),		
CC	SEK-1 (not defined) and STG (not defined) polypeptides, and the		
CC	polynucleotides encoding them. All three genes were identified due to		
CC	their proximity to the human leukocyte antigen C (HLA C) locus on		
CC	chromosome 6. The HLA Cw6 allele is associated with psoriasis and as the		
CC	three genes are expressed in normal skin and/or keratinocyte tissue, they		
CC	may also have a role in psoriasis. Psoriasis is a chronic inflammatory		
CC	dermatosis that is characterised by hyperproliferation of epidermal		
CC	cells. Possible treatments against psoriasis involve the inhibition of		
CC	movement of cells into the epidermis, or the inhibition of		
CC	hyperproliferation or abnormal differentiation of keratinocytes, by the		
CC	inhibition of the CAN-1, STG or SEK-1 polypeptides binding to their		
CC	binding partners. The polypeptides are useful for diagnosing or		
CC	predicting the susceptibility to psoriasis in an individual, for		

CC ameliorating the symptoms and/or progression of psoriasis and for
 CC identifying agents useful for treating psoriasis or modulating the
 CC activity of the polypeptide. The polypeptides are also useful for
 CC enhancing the level of CAN-1, STG or SEEK-1 biological activity in a cell
 CC or tissue. The nucleic acid molecules are useful as hybridisation probes
 CC in diagnostic procedures (such as diagnosing the presence of psoriasis or
 CC the propensity to develop psoriasis) and for suppressing the expression
 CC of CAN-1 or STG gene (e.g. antisense inhibition, gene therapy).
 CC Antibodies, raised against the polypeptides, are useful for decreasing
 CC the level of CAN-1, STG or SEEK-1 biological activity in a cell. The
 CC sequence presented is the human candidate coding sequence-1 (CAN-1)
 CC deletion polymorphism genomic DNA
 XX
 SQ Sequence 2997 BP; 617 A; 785 C; 913 G; 682 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 7,53e-24 Length: 2997
 Score: 692.00 Matches: 114
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-994-365-3 (1-114) x ABR86967 (1-2997)
 QY 1 SerGluGlyHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThr 20
 Db 2213 AGCGAGGGCCACCCCTCTCACACCGCAGAGAGCGAGAGGAGGAGGTCCCAACA 2272
 QY 21 LeuProGluGlyProProValProGlyAspProTrpProGlyAlaProProLeuPheGlu 40
 Db 2273 TTGGCTCAGGGGCCCCCAAGTCCCGGTGACCTTGGCGAGGGGCAACCCCTCTTGGAA 2332
 QY 41 AspProProProTrpArgProSerArgProTrpArgAspLeuProGluTrpValTrp 60
 Db 2333 GATCTCCGCTACCCGCCAGTCGTCCTGGAGAGACCTGCTGAACTGGAGTCTGG 2392
 QY 61 ProProGluProProArgTrpHisAspProProGluProProArgProAspAspProTrpPro 80
 Db 2393 CCCCTCAACCGCTAGAACGATCTCTCAACCTCCCGGCTGACGACCTTGGCCG 2452
 QY 81 AlaGlyProGluProProGluAspProTrpProProAlaProGluValAspAspArgPro 100
 Db 2453 GCAGAGACCCAGCCGCCAGAAACCCCTGCGCTCTCCCTGAGGTGAGCAACCGACCT 2512
 QY 101 GlnGluGluProAspLeuAspAspProProArgGluGluTrpArg 114
 Db 2513 CAGGAGAGCCAGACCTTAGACCCGCCGGAAGATACAGA 2554
 RESULT 4
 ABR86963 standard; DNA; 3001 BP.
 XX ABR86963;
 AC
 XX
 DT 24-SEP-2002 (first entry)
 XX
 DE Human candidate coding sequence-1 (CAN-1) genomic DNA.
 XX
 KM Human; antipsoriatic; chromosome 6; candidate coding sequence-1; CAN-1;
 KM SEEK-1; STG; human leukocyte antigen C; HLA C; HLA Cw6; psoriasis; skin;
 KM keratinocyte; chronic inflammatory dermatosis; erythroderma; seborrheic;
 KM guttate; pustular variant; Reiter's disease; hyperproliferation;
 KM epidermis; differentiation; diagnosis; gene therapy; gene; ds; SNP;
 KM single nucleotide polymorphism; deletion polymorphism.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT variation replace(11..16,CA)
 FT /tag= a
 FT /note= "Deletion polymorphism"
 FT variation replace(118,T)

FT FT /*tag= b
 FT FT /standard_name= "Single nucleotide polymorphism"
 FT FT replace(554,A)
 FT FT /*tag= c
 FT FT /standard_name= "Single nucleotide polymorphism"
 FT FT replace(1100,T)
 FT FT /*tag= d
 FT FT /standard_name= "Single nucleotide polymorphism"
 FT FT replace(1700,A)
 FT FT /*tag= e
 FT FT /standard_name= "Single nucleotide polymorphism"
 FT FT replace(1394,T)
 FT FT /*tag= f
 FT FT /standard_name= "Single nucleotide polymorphism"
 FT FT 1485..2561
 FT FT /*tag= g
 FT FT /product= "CAN-1"
 FT FT 1485..1539
 FT FT /*tag= h
 FT FT /number= 1
 FT FT 1540..2205
 FT FT /*tag= i
 FT FT /number= 1
 FT FT replace(1681,A)
 FT FT /*tag= j
 FT FT /standard_name= "Single nucleotide polymorphism"
 FT FT replace(1879,T)
 FT FT /*tag= k
 FT FT /standard_name= "Single nucleotide polymorphism"
 FT FT replace(1586,A)
 FT FT /*tag= l
 FT FT /standard_name= "Single nucleotide polymorphism"
 FT FT replace(2020,C)
 FT FT /*tag= m
 FT FT /standard_name= "Single nucleotide polymorphism"
 FT FT replace(2111,G)
 FT FT /*tag= n
 FT FT /standard_name= "Single nucleotide polymorphism"
 FT FT 2206..2561
 FT FT /*tag= o
 FT FT /number= 2
 FT FT replace(2397,T)
 FT FT /*tag= p
 FT FT /standard_name= "Single nucleotide polymorphism"
 FT FT replace(2655,G)
 FT FT /*tag= q
 FT FT /standard_name= "Single nucleotide polymorphism"
 FT FT replace(2822,G)
 FT FT /*tag= r
 FT FT /standard_name= "Single nucleotide polymorphism"
 FT FT replace(2875,C)
 FT FT /*tag= s
 FT FT /standard_name= "Single nucleotide polymorphism"
 FT FT
 FT WO200244375-A2.
 FT PD
 FT PD 06-JUN-2002.
 FT PD
 FT PF 27-NOV-2001; 2001WO-US044506.
 FT XX
 XX PR 28-NOV-2000; 2000US-0253592P.
 XX PR 15-DEC-2000; 2000US-0256839P.
 XX XX
 PA (CELL-) CELLTECH R & D INC.
 XX
 PI Charmley P, Mose P, Meeuen M;
 XX
 XX MPI; 2002-508513/54.
 DR P-PSDB; AAU79579.
 XX
 PT Novel isolated CAN-1 polypeptide involved in keratinocyte proliferation
 PT and differentiation, and polynucleotides encoding the polypeptide, useful
 PT for diagnosing or predicting susceptibility to psoriasis in individual.

Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 4
 Gaps: 0

Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-09-994-365-3 (1-114) x AAH45310 (1-25235)

QY 1 SerGluGlyHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThr 20
 DB 1766 AGCGAGGGCCACCCCTCTCAACCCGACGAGAGCGAGGAGGCTCCCAACA 1825
 QY 21 LeuProGluGlyProProValProGlyAspProTyrProGlyAlaProProLeuPheGlu 40
 DB 1826 TTGCTCAGGGGCCCCCAAGTCCCGTGACCTTGAGCGAGGAGGACCCCTCTTTGAA 1885
 QY 41 AspProProProThrArgProSerArgProTyrPArgAspLeuProGluThrGlyValTyr 60
 DB 1886 GATCCTCGGCTACCCGCCAGTCTCTCCGAGAGACCTGCTGAACTGAGAGTCTGG 1945
 QY 61 ProProGluProProArgThrAspProProGluProProArgProAspAspProTyrPro 80
 DB 1946 CCCCTCAACCGCTAGAACGATCTCTCAACCTCCCGGCTTGACGACCTTGAGCGG 2005
 QY 81 AlaGlyProGluProProGluAsnProTyrProProAlaProGluValAspAsnArgPro 100
 DB 2006 GCAGAGACCCCAAGCCCAAGAAACCCCTGCTCTGCCCCCTGAGTGAGCAACCGACT 2065
 QY 101 GlnGluGluProAspLeuAspProProArgGluGluTyrArg 114
 DB 2066 CAGAGAGACCGACACTAGACCCGCCGGAAGAGTACAGA 2107

RESULT 6

ABQ75680 standard; DNA; 55050 BP.

ABQ75680:

11-NOV-2002 (first entry)

Human SEEK1 consensus genomic DNA.

Human; SEEK1; chromosome 6p21; inflammatory disease; antiinflammatory;
 antipsoriatic; gene therapy; gene; ds.

Homo sapiens.

WO200264831-A2.

22-AUG-2002.

13-FEB-2002; 2002WO-GB000653.

13-FEB-2001; 2001GB-00003514.

(OXAG-) OXAGEN LTD.

Lench NJ, Allen MJ, Nicholls RK;

WPI; 2002-667013/71.

Polymorphisms in the SEEK1 gene and polynucleotides encoding the SEEK1
 gene, for treating, diagnosing or determining susceptibility to SEEK1
 mediated disease, e.g. inflammatory disease such as psoriasis.

Claim 4; Fig 2; 69bp; English.

The present invention describes a polynucleotide (I) comprising: (a) a
 nucleic acid sequence (II) encoding the SEEK1 gene; (b) a nucleic acid
 sequence (III) encoding a fragment of the SEEK1 gene; or (c) a nucleic
 acid sequence (IV) that hybridises under stringent conditions to the
 polynucleotide of (II) or (III). (I) has antiinflammatory and
 antipsoriatic activities and can be used in gene therapy. The alleles of
 one or more polymorphisms in the SEEK1 gene can be used for the

CC manufacture of a medicament for the diagnosis and treatment of SEEK1
 CC mediated disease. SEEK1 protein fragments are useful in diagnostic,
 CC prognostic or therapeutic methods, or as research tools in drug
 CC screening. Human SEEK1 is located to chromosome 6p21. The present
 CC sequence represents a human SEEK1 nucleotide sequence

XX Sequence 55050 BP; 13076 A; 14198 C; 14560 G; 13197 T; 0 U; 19 Other;

Alignment Scores:

Pred. No.: 7, 11e-23 Length: 55050

Score: 692.00 Matches: 114

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-994-365-3 (1-114) x ABQ75680 (1-55050)

QY 1 SerGluGlyHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThr 20
 DB 27111 AGCGAGGGCCACCCCTCTCAACCCGACGAGAGCGAGGAGGCTCCCAACA 27170
 QY 21 LeuProGluGlyProProValProGlyAspProTyrProGlyAlaProProLeuPheGlu 40
 DB 27171 TTGCTCAGGGGCCCCCAAGTCCCGTGACCTTGAGCGAGGAGGACCCCTCTTTGAA 27230
 QY 41 AspProProProThrArgProSerArgProTyrPArgAspLeuProGluThrGlyValTyr 60
 DB 27231 GATCCTCGGCTACCCGCCAGTCTCTCCGAGAGACCTGCTGAACTGAGAGTCTGG 27290
 QY 61 ProProGluProProArgThrAspProProGluProProArgProAspAspProTyrPro 80
 DB 27291 CCCCTCAACCGCTAGAACGATCTCTCAACCTCCCGGCTTGACGACCTTGAGCGG 27350
 QY 81 AlaGlyProGluProProGluAsnProTyrProProAlaProGluValAspAsnArgPro 100
 DB 27351 GCAGAGACCCCAAGCCCAAGAAACCCCTGCTCTGCCCCCTGAGTGAGCAACCGACT 27410
 QY 101 GlnGluGluProAspLeuAspProProArgGluGluTyrArg 114
 DB 27411 CAGAGAGACCGACACTAGACCCGCCGGAAGAGTACAGA 27452

RESULT 7

ACH72505 standard; DNA; 565 BP.

ACH72505:

29-JUL-2004 (first entry)

Human genome derived single exon probe #5700.

Human; probe; ss; gene expression; single exon probe; microarray;

alternative splicing event; genomic alteration.

Homo sapiens.

US2003194704-A1.

16-OCT-2003.

03-APR-2002; 2002US-00029386.

03-APR-2002; 2002US-00029386.

(PENN/) PENN S G.

(RANK/) RANK D R.

(HANSZ/) HANSZEL D K.

Penn SG, Rank DR, Hanzel DK;

WPI; 2004-119264/12.

PT New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.

PS Claim 15; SEQ ID NO 5700; 80pp; English.

XX
 CC The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 688 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridizes under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subsequence, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above, the probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterizing
 CC alternative splicing events, in detecting and characterizing gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20030194704
 XX

XX Sequence 565 BP; 99 A; 227 C; 112 G; 127 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.16e-15	Length:	565
Score:	486.00	Matches:	79
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	70.23%	Indels:	0
DB:	12	Gaps:	0

US-09-994-365-3 (1-114) x ACH72505 (1-565)

QY 36 ProProLeuPheGluAaPProPProPProThArGProSeArAProTPaAaPleuPro 55
 DB 1 CCCCCTCTCTTGAAGATCCTCGCCCTAACCCGCCAGTGCTGCTTGAAGACCTGCT 60
 QY 56 GluThGlyValTPProPProGluPProArGThArPProPProGluPProArGPro 75
 DB 61 GAAACGTGAGTCTGGCCCCCTGAACCCGCTGAAGAGATCTCTCAACTCCCCGGCCT 120
 QY 76 AsPaSPProTrPProAlaGlyPProGluPProGluAaPProTPPProPProAlaPProGlu 95
 DB 121 GAGGACCTTGGCGGAGAGACCCCAACCAAAACCCCTGCTGCTGCGCCCTGAG 180
 QY 96 ValAsPaSPaArPProGluGluPProAsPleuAaPProPProAaGluGluTPArG 114
 DB 181 GTGAGCAACGAGACTCAGAGAGACCAAGACTTACCCACCCCGGAGAGATACAGA 237

RESULT 8
 ACH86315

ID ACH86315 standard; DNA; 157 BP.

XX ACH86315;

AC 29-JUL-2004 (first entry)

DE Human genome derived single exon probe #19510.

KW Human; probe; aa; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.

XX Homo sapiens.

PN US2003194704-A1.

XX 16-OCT-2003.

XX 03-APR-2002; 2002US-00029386.

XX 03-APR-2002; 2002US-00029386.

XX (PENN/) PENN S G.

PA (RANK/) RANK D R.

PA (HANZ/) HANZEL D K.

PI Penn SG, Rank DR, Hanzel DK;

XX WPI; 2004-119264/12.

PT New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.

PS Claim 1; SEQ ID NO 19510; 80pp; English.

XX
 CC The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 688 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridizes under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subsequence, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above, the probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterizing
 CC alternative splicing events, in detecting and characterizing gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20030194704
 XX

XX Sequence 157 BP; 38 A; 64 C; 38 G; 17 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,45e-07	Length:	157
Score:	314.00	Matches:	51
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	45.38%	Indels:	0
DB:	12	Gaps:	0

US-09-994-365-3 (1-114) x ACH66315 (1-157)

QY 64 ProProArgThrAspProProGlnProProArgProAspAspProTTPProAlaGlyPro 83
DB 2 CCGCCTAGAAAGGATCCTCTCAACCTCCCGGCTGACACCCCTTGCCGCGAGGAGCC 61
QY 84 GlnProProGlnAspProTTPProProAlaProGluValAspAspAspArgProGlnGlu 103
DB 62 CAGCCCCCAAGAAACCCCTGCTCCCTGAGGTGACCAACGACCTCAGAGAGAG 121
QY 104 ProAspLeuAspProProArgGluGluTyrArg 114
DB 122 CCAGACTAGACCCACCCCGGGAAGGTACAGA 154

RESULT 9
ACA43990/c
ID ACA43990 standard; DNA; 711 BP.

XX ACA43990;

XX 19-JUN-2003 (first entry)

XX Prokaryotic essential gene #25647.

XX Antisense; ds; prokaryotic essential gene; cell proliferation;
XX drug design; gene.

XX Pseudomonas putida.

XX MO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Foreyth RA, Xu HH;
XX P-PsDB; ABU40120.XX WPI; 2003-029926/02.
XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.

XX Claim 14; SEQ ID NO 31860; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 711 BP; 120 A; 161 C; 304 G; 126 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.165	Length:	711
Score:	199.00	Matches:	46
Percent Similarity:	44.95%	Conservative:	3
Best Local Similarity:	42.20%	Mismatches:	42
Query Match:	28.76%	Indels:	18
DB:	8	Gaps:	6

US-09-994-365-3 (1-114) x ACA43990 (1-711)

QY 5 ProSerHisProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGly 24
DB 446 CCGGCATGGCCACACCG-----TCACCGCGCGTGGCG--TGG 411
QY 25 ProProValPro--GlyAspProTTPProGlyAlaProProLeuHeuGluAspProPro 43
DB 410 CCACCACTTCCTCCGCCACCATGACCGCCGCCACCACTT-----CCACCA 357
QY 44 ProThrArgProSerArgProTTPArgAspLeuProGluThrGlyValTTPProGlu 63
DB 356 CCGTGGCCACACACCGCGCGCTTCCACCAACCGG-----TGGCCACCGCCA 309
QY 64 ProProArgThrAsp-----ProProGlnProProArgProAspAspProTTPPro 80
DB 308 CCGCGCTTCCACCAACCGGTGACCAACCGCGCGCTTCCACCGCCACCGGTGACCA 249
QY 81 AlaGlyProGlnProProGluAspProTTPProProAlaProGluValAspAspArgPro 100
DB 248 CCGCGCGCGCGCTTCCGCCACCGGTGACCAACCGCGCGCGCTTCCACCGCCACCG 189
QY 101 GlnGluGluProAspLeuAspProPro 109
DB 188 TGGCCACCGCCACCGCCACCGCCACCG 162

RESULT 10
ACA40420/c
ID ACA40420 standard; DNA; 2772 BP.

XX ACA40420;

XX 19-JUN-2003 (first entry)

XX Prokaryotic essential gene #22077.

XX Antisense; ds; prokaryotic essential gene; cell proliferation;
XX drug design; gene.

XX Mycobacterium tuberculosis.

[illegible][illegible]

Qy 83 -----ProglInProgluAsnProTTPProProAlaProgluValAspAsnArg 99
 Db 91065 CCGAGACCCCAAGTCCGCCGAGCCACCTGCGCGGACACCAACCGTTG----- 91015
 Qy 100 ProglIngluProAspLeuAspPro 108
 Db 91014 CCGAATAGCAGCCGCGCTTGCCGCCG 90988

RESULT 13
 AAI23276/c
 ID AAI23276 standard; DNA; 446 BP.
 XX
 AC AAI23276;
 XX
 DT 12-OCT-2001 (first entry)
 XX
 DE Probe #13209 for gene expression analysis in human cervical cell sample.
 XX
 KW Probe; human; microarray; gene expression; cervical epithelial cell;
 KM cervical cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200157278-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000670.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488901/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human cervical epithelial cells.
 XX
 PS Claim 25; SEQ ID NO 13209; 487bp; English.
 XX
 CC The present invention relates to human single exon nucleic acid probes
 CC (SENPs). The present sequence is one such probe. The SENPs are derived
 CC from human HeLa cells. The SENPs can be used to produce a single exon
 CC microarray, which can be used for measuring human gene expression in a
 CC sample derived from human cervical epithelial cells. By measuring gene
 CC expression, the probes are therefore useful in grading and/or staging of
 CC diseases of the cervix, notably cervical cancer. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 446 BP; 31 A; 26 C; 254 G; 135 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0.285 Length: 446
 Score: 190.50 Matches: 43
 Percent Similarity: 40.00% Conservative: 1
 Best Local Similarity: 39.09% Mismatches: 57
 Query Match: 27.53% Indels: 9
 DB: 4 Gaps: 2

US-09-994-365-3 (1-114) x AAI23276 (1-446)
 Qy 5 ProSeRtAspProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGly 24

Db 403 CCACACACACACACACATCATCACCAACCAACCATCATCACACACACACATCA 344
 Qy 25 ProProValProGlyAspProTTPProGlyAlaProProLeuPheGluAspProPro 44
 Db 343 CCACACACACACACATCATCACCAACCAACCATCATCATCACACACACATCA 284
 Qy 45 ThrArgProSeRtAspProTTPArgAspLeuProGluThrGlyValTTPProProGluPro 64
 Db 283 CCACACACATCATCACACATCATCATCATCATCA-----CCACACACACCA 236
 Qy 65 ProArgThrAspProProGlnProProArgProAspAspProTTPProAlaGlyProGln 84
 Db 235 CCACATCATCACACACACACATCATCATCATCATCATCATCATCATCATCATCA 176
 Qy 85 ProProGluAsnProTTPPro-----ProAlaProGluValAspAsnArg 99
 Db 175 CCACACACACACACATCATCATCATCATCATCATCATCATCATCATCATCATCA 116
 Qy 100 ProglIngluProAspLeuAspProPro 109
 Db 115 CCGCGCGCACCATCGCATGCGCACCGCCA 86

RESULT 14
 ABA68382/c
 ID ABA68382 standard; DNA; 446 BP.
 XX
 AC ABA68382;
 XX
 DT 01-FEB-2002 (first entry)
 XX
 DE Human foetal liver single exon nucleic acid probe #16687.
 XX
 KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
 KM Homo sapiens.
 XX
 OS Homo sapiens.
 XX
 PN WO200157277-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000669.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-483447/52.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human fetal liver.
 XX
 PS Claim 4; SEQ ID NO 16687; 639bp + Sequence Listing; English.
 XX
 CC The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human fetal liver. The
 CC present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 446 BP; 31 A; 26 C; 254 G; 135 T; 0 U; 0 Other;

Alignment Scores:
 SQ

Pred. No.: 0.285 Length: 446
 Score: 190.50 Matches: 43
 Percent Similarity: 40.00% Conservative: 1
 Best Local Similarity: 39.09% Mismatches: 57
 Query Match: 27.53% Indels: 9
 DB: 4 Gaps: 2

US-09-994-365-3 (1-114) x ABA68382 (1-446)

QY 5 ProSerHisProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGly 24
 DB 403 CCACCACACACACACATCACACACACACACACACACATCACACACACATCA 344
 QY 25 ProProValProGlyAspProTrpProGlyAlaProProLeuPheGluAspProPro 44
 DB 343 CCACCACACACACATCACACACACACACACACACATCACACACACATCA 284
 QY 45 ThrArgProSerArgProTrpArgAspLeuProGluThrGlyValTrpProProGluPro 64
 DB 283 CCACCACACACACATCACACATCACATCACACCA-----CCACCACACCA 236
 QY 65 ProArgThrAspProGlnProProArgProAspAspProTrpProAlaGlyProGln 84
 DB 235 CCACCATCACACACACACACACACATCACACACACACATCACACATCA 176
 QY 85 ProProGluAsnProTrpPro-----ProAlaProGluValAspAsnArg 99
 DB 175 CCACCACACACACATCACATCACATCACATCACATCACATCACATCA 116
 QY 100 ProGlnGluGluProAspLeuAspProPro 109
 DB 115 CCGCGCGCACACCGCATGCGCACCGCCA 86

RESULT 15
 AAI48596/c
 ID AAI48596 standard; DNA; 446 BP.
 XX

AC AAI48596;

DT 17-OCT-2001 (first entry)

XX Probe #17282 used to measure gene expression in human placenta sample.

XX Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder; se.

XX Homo sapiens.

XX W0200157272-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000663.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human placenta.

XX Claim 25; SEQ ID NO 17282; 654bp; English.

CC The present invention relates to single exon nucleic acid probes (SENP).
 CC The present sequence is one such probe. The probes are useful for
 CC producing a microarray for predicting, measuring and displaying gene
 CC expression in samples derived from human placenta. The probes are useful
 CC for antenatal diagnosis of human genetic disorders

XX SQ Sequence 446 BP; 31 A; 26 C; 254 G; 135 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.285 Length: 446
 Score: 190.50 Matches: 43
 Percent Similarity: 40.00% Conservative: 1
 Best Local Similarity: 39.09% Mismatches: 57
 Query Match: 27.53% Indels: 9
 DB: 4 Gaps: 2

US-09-994-365-3 (1-114) x AAI48596 (1-446)

QY 5 ProSerHisProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGly 24
 DB 403 CCACCACACACACATCACACACACACACACACACATCACACACACATCA 344
 QY 25 ProProValProGlyAspProTrpProGlyAlaProProLeuPheGluAspProPro 44
 DB 343 CCACCACACACACATCACACACACACACACACACATCACACACACATCA 284
 QY 45 ThrArgProSerArgProTrpArgAspLeuProGluThrGlyValTrpProProGluPro 64
 DB 283 CCACCACACACACATCACATCACATCACATCACACCA-----CCACCACACCA 236
 QY 65 ProArgThrAspProGlnProProArgProAspAspProTrpProAlaGlyProGln 84
 DB 235 CCACCATCACACACACACACACATCACACACACACATCACACATCA 176
 QY 85 ProProGluAsnProTrpPro-----ProAlaProGluValAspAsnArg 99
 DB 175 CCACCACACACACATCACATCACATCACATCACATCACATCACATCA 116
 QY 100 ProGlnGluGluProAspLeuAspProPro 109
 DB 115 CCGCGCGCACACCGCATGCGCACCGCCA 86

Search completed: January 11, 2005, 12:05:14
 Job time : 402.064 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_p2n model

Run on: January 11, 2005, 10:41:32 / Search time 3096.24 Seconds
(without alignments)
1741.152 Million cell updates/sec

Title: US-09-994-365-3
Perfect score: 692
Sequence: 1 SEGHPHPAEDREAGSPF.....EVDNRQEPDLPDPREYR 114

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame_p2n.model -DEV=rlh
-Q=cgnt2_1/USFTO.spool_n/US09994365/turnat_10012005_172231.6821/app.query.fasta_1.590
-DB=Genembi -QFMT=faetap -SUFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USBR=US09994365.ccgnt2_1.1.3851@turnat_10012005_172231.6821 -NCPD=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Genembi: *
1: gb_da: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pac: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	692	100.0	891	AX477387 Sequence
2	692	100.0	1143	CQ722444 Sequence
3	692	100.0	1143	AB031480 Sequence
4	692	100.0	1185	AF484420 Homo sapi

5	692	100.0	1473	AX406002 Sequence
6	692	100.0	2997	AX477396 Sequence
7	692	100.0	3001	AX477390 Sequence
8	692	100.0	25235	BD095297 The metho
9	692	100.0	30911	AB088114 Homo sapi
10	692	100.0	39196	AB023060 Homo sapi
11	692	100.0	40878	AC004195 Homo sapi
12	692	100.0	55050	AC522117 Sequence
13	692	100.0	70288	AL662867 Human DNA
14	692	100.0	99999	AP000510 Homo sapi
15	692	100.0	113388	AL773544 Human DNA
16	692	100.0	135396	BX927139 Human DNA
17	692	100.0	204238	AL662844 Human DNA
18	692	98.6	175689	AC148703 Macaca mu
19	666	95.7	300050	AB100083 Pan trogl
20	652	94.2	200068	AC148691 Macaca mu
21	568	82.1	154749	AB113354 Sus scrof
22	541	78.2	383	AF484422 Sus scrof
23	507.5	73.3	349571	BX883047 Rattus no
24	506	73.1	773	AF159091 Mus muscu
25	506	73.1	809	AF484421 Mus muscu
26	506	73.1	1377	AF159090 Mus muscu
27	506	73.1	159179	AF111103 Mouse maj
28	506	73.1	126594	AC087216 Mus muscu
29	441	63.7	349980	AX344554 Sequence
30	304.5	44.0	248	AR418279 Sequence
31	304.5	44.0	248	AX978973 Sequence
32	304.5	44.0	248	BD113832 EST and e
33	258	37.3	388	BD113832 Human HLA c
34	210.5	30.4	164520	AC020738 Homo sapi
35	210	30.3	247221	BX470211 Dario rer
36	208	30.1	185549	BX927317 Dario rer
37	207.5	30.0	152340	CR396595 Dario rer
38	206.5	29.8	91040	BX246094 Zebrafish
39	206.5	29.8	166514	BX469924 Zebrafish
40	205	29.6	177205	CR376782 Dario rer
41	205	29.6	185411	CR376782 Dario rer
42	205	29.6	225024	CR394539 Dario rer
43	204.5	29.6	155657	CR394539 Dario rer
44	204	29.5	242992	BX469901 Dario rer
45	203.5	29.4	161366	BX567998 Dario rer

ALIGNMENTS

RESULT 1	AX477387	891 bp	DNA	linear	PAT 12-AUG-2002
LOCUS	AX477387				
DEFINITION	Sequence 1 from Patent WO0244375.				
ACCESSION	AX477387				
VERSION	AX477387.1	GI:22216617			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Charnley, P., Moss, P. and Mceuen, M.				
AUTHORS	Charnley, P., Moss, P. and Mceuen, M.				
TITLE	Compositions and methods for diagnosing or treating psoriasis				
JOURNAL	Patent: WO 0244375-A 1 06-JUN-2002;				
CELL	Celltech R & D, Inc. (US)				
FEATURES	location/Qualifiers				
source	1. 891				
	/organism="Homo sapiens"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
	64..474				
	/note="unnamed protein product"				
	/codon_start=1				
	/protein_id="CAD43680.1"				
	/db_xref="GI:22216618"				
	/translation="MTLNKLTGILVLCITRIGSGEGHPHPAEDREAGSPFLP				
	QGPVPQDPPWGPAPLFEEDPPTRPSPRMRDLPEGTVMPEPEPTDPPQPPRDDPWP				

Alignment Scores:
Pred. No.: 6 56e-20 Length: 1143
Score: 692.00 Matches: 114
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-994-365-3 (1-114) x AB031480 (1-1143)

Qy 1 SerGIuGIyHISProSerHISProProAlaGIuAPArGIuGIuAlaGIySerProThr 20
Db 382 AGGAGGGGCCACCCCTCTCAACCCGACAGAGACCGAGAGGAGGAGGCTCCCAACA 441

Qy 21 LeuProGIuGIyProProValProGIyAspProTyrProGIyAlaProProLeuPheGlu 40
Db 442 TTGCTCAGGGGCCCCCAAGTCCCGGTGACCTTGGCCAGGGGCAACCCCTCTTTGAA 501

Qy 41 AspProProThrArGIyProSerArGIyProTyrArGIyAspLeuProGIuThrGIyValTyr 60
Db 502 GATCTCTGGCTACCCGCCCAAGTCTCCGTGAGAGACCTGCTGAACCTGAGTCTGG 561

Qy 61 ProProGIuProProArGIyThrAspProProGIuProProArGIyProAspAspProTyrPro 80
Db 562 CCCCCTGAAACGGCTAGAGGAGATCTCTCAACCTCCCGGCTGAGACCTTGGCCG 621

Qy 81 AlaGIyProGIuProProGIuAspProTyrProProAlaProGIuValaAspAsnArGIyPro 100
Db 622 GCAGAGCCCAAGCCCAAGAAACCTCGGCTCTCCCTCGAGTGAACAACCGACT 681

Qy 101 GIuGIuGIuProAspLeuAspProProArGIyGIuGIyTyrArGIy 114
Db 682 CAGAGAGCCAGACCTAGACCCACCCGGAGAGATGACAGA 723

RESULT 4
AF484420 1185 bp mRNA linear PRI 02-MAR-2003
LOCUS Homo sapiens psoriasis susceptibility 1 candidate 2 (PSORS1C2)
DEFINITION mRNA, complete cds.
ACCESSION AF484420
VERSION AF484420.1 GI:2862834
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Holm,S.J., O'Brien,K.P., Carlen,L. and Stahle-Backdahl,M.
TITLE The PSORS1C1 and PSORS1C2 genes in 6p21.3 associate strongly with
psoriasis in the Swedish population
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 1185)
TITL Holm,S.J., O'Brien,K.P., Carlen,L. and Stahle-Backdahl,M.
JOURNAL Direct Submission
SUBMITTED (15-FEB-2002) Dermatology, Karolinska Institute, L8:02
Karolinska Sjukhuset, Stockholm S-17176, Sweden
FEATURES
SOURCE Location/Qualifiers
1. 1185
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
/tissue_type="skin"
1. 1185
/gene="PSORS1C2"
325..735
/gene="PSORS1C2"
/codon_start=1
/product="psoriasis susceptibility 1 candidate 2"
/protein_id="AA049377.1"
/db_xref="GI:2862835"

ORIGIN
/translation="MILNKKLIGILVCLHTRGISGSGHSPHPADREAGSPPLP
OGPPVGDPPWPGAPPLFEDPPPTPRSPRPMDDLEETGWWPEPEPRTDPPQPPRDDPWP
AGQPPEPNPWPAPBYVDNRPQSEPDLDPREEYR"

Alignment Scores:
Pred. No.: 6 73e-20 Length: 1185
Score: 692.00 Matches: 114
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-994-365-3 (1-114) x AF484420 (1-1185)

Qy 1 SerGIuGIyHISProSerHISProProAlaGIuAPArGIuGIuAlaGIySerProThr 20
Db 391 AGGAGGGGCCACCCCTCTCAACCCGACAGAGACCGAGAGGAGGAGGCTCCCAACA 450

Qy 21 LeuProGIuGIyProProValProGIyAspProTyrProGIyAlaProProLeuPheGlu 40
Db 451 TTGCTCAGGGGCCCCCAAGTCCCGGTGACCTTGGCCAGGGGCAACCCCTCTTTGAA 510

Qy 41 AspProProThrArGIyProSerArGIyProTyrArGIyAspLeuProGIuThrGIyValTyr 60
Db 511 GATCTCTGGCTACCCGCCCAAGTCTCCGTGAGAGACCTGCTGAACCTGAGTCTGG 570

Qy 61 ProProGIuProProArGIyThrAspProProGIuProProArGIyProAspAspProTyrPro 80
Db 571 CCCCCTGAAACGGCTAGAGGAGATCTCTCAACCTCCCGGCTGAGACCTTGGCCG 630

Qy 81 AlaGIyProGIuProProGIuAspProTyrProProAlaProGIuValaAspAsnArGIyPro 100
Db 631 GCAGAGCCCAAGCCCAAGAAACCTCGGCTCTCCCTCGAGTGAACAACCGACT 690

Qy 101 GIuGIuGIuProAspLeuAspProProArGIyGIuGIyTyrArGIy 114
Db 691 CAGAGAGCCAGACCTAGACCCACCCGGAGAGATGACAGA 732

RESULT 5
AX406002 1473 bp DNA linear PAT 14-JUN-2002
LOCUS AX406002
DEFINITION Sequence 417 from Patent WO0222660.
ACCESSION AX406002
VERSION AX406002.1 GI:21439443
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Tang,Y.T., Liu,C., Zhou,P., Asundi,V., Zhang,J., Zhao,Q.A., Ren,F.,
Xue,A.J., Yang,Y., Wehrman,T. and Dymnac,R.T.
TITLE Novel nucleic acids and polypeptides
JOURNAL Patent: WO 0222660-A 417 21-MAR-2002;
HYSBO, INC. (US)
FEATURES
SOURCE Location/Qualifiers
1. 1473
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
636..1046
/note="unamed protein product"
/codon_start=1
/protein_id="CAD35109.1"
/db_xref="GI:21439444"
/translation="MILNKKLIGILVCLHTRGISGSGHSPHPADREAGSPPLP
OGPPVGDPPWPGAPPLFEDPPPTPRSPRPMDDLEETGWWPEPEPRTDPPQPPRDDPWP
AGQPPEPNPWPAPBYVDNRPQSEPDLDPREEYR"

ORIGIN
Alignment Scores:
Pred. No.: 7.88e-20 Length: 1473

Score:	692.00	Matches:	11
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-994-365-3 (1-114) x AX406002 (1-1473)

Qy 1 SerGluGlyHisProSerHisProProAlaGlnspargLuglAlaGlySerProThr 20
Db 702 AGCGAGGGCCACCTCTCACCACCCGCAGAGGACCGAGAGGAGGCCAGGCTCCCCACA 76

0y 21 LeuProGInglyProProValProGlyaspProTirProGlyalaProProleuPheGu 40
|||
Db 762 TTGCCTCAGGGCCCCCCAGTATCCCGGTGACCTTGCCACAGGGGCACCCCCTTCCTTTGA 82

4. AspProProThrArgProSerArgProIpargaspleuroglinThrGlyValTyr 60
 |||||
 822 GATCTCTCGGCTACCGGCCCAAGTCGTCCCTGAGAGAACCTGCTGAACCTGAGAGTCTGG 88

[illegible]

Dy 81 A I G S I Y P R O G I N P R O F I G I U A S H R T I P R O P C L A E P R O G I U V a l J a p a s n y g P r o 100
| | | | |
Db 942 G C A G A C C C C A G C C C C A G A A A A C C C C T G G C T C T G C C C C T G A G S T G A C A C C G A C C T 100

	lv1	gmgngugnufrfoasbleuaspproproargluginutyrarg	114
Db	1002	cagcagagaccagacctagacccacccccgggaagactacaga	1043

AX477396	AX477396	2997 bp	DNA	linear	PAT 12-AUG-2002
LOCUS	Sequence	10 from Patent WO0244375.			
DEFINITION					

VERSION	AX477396.1	GI:22216625
KEYWORDS		
SOURCE	Homo sapiens (human)	

REFERENCE
1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE Compositions and methods for diagnosing or treating psoriasis
JOURNAL Patent: WO 0244375-A 10 06-UUN-2002;
Celltech R & D, Inc. (US)

```
source
1. .2997
/organism="Homo sapiens"
/mol_type="unassigned DNA"
```

ORIGIN

Alignment Scores:

Score:	692.00	Matches:	114
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

DB: 6 Gap
US-09-994-365-3 (1-114) X AX477396 (1-2997)

QY 1 SerGIUGLHIHisProSerHisProProAlaGIuAspAGLUGLualaGlySerProThr 20
 Db 2213 AGCGAGGCGCACCCCTCTCACCCACCGCAGAGGACCGAGAGGAGCAGGCTCCCCACA 22

QY 21 LEUPROGLINGLYPROPROVALPROGLYASPPROTTPROGLYLALAPROLEUHEGU 40
|||||
Db 2273 TTGCTCAGGGCCCCCAGTCCCGGTACCCCTTGCCAGGGGGACCCCCTCTTTGA 2337

QY 41 AspProProThrArgProSerArgProTPrArgAspLeuProGluThrGlyValTrp 600
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 2333 GATCTTCGGCCTACCGCCCAAGTCGTCCCTGGAGAGACTGTGCCTGAACCTGGAGTTCTGG 2333

Qy	61	Pro	Pro	Glu	Pro	Pro	Arg	Thr	Asp	Pro	Gln	Pro	Pro	Arg	Pro	Asp	Asp	Pro	Trp	Pro	80
Dp	2393	CCCC	TGA	ACG	CTA	GAA	CGA	TCT	CTC	CTA	CACT	CCCC	GGC	CTG	ACA	GAC	ACC	CTT	GGC	CC	2452

QY 81 A I A G I P R O G I N P R O G I U A N P S C R T P P R O C I A L A P R O G I U V A L A S P A S M A R G P C 100

Db 2453 G C A G A C C C A G C C C C C A G A A A A C C C T G G C C T C T G C C C C T A G A G T G C A C A C C G A C T 2512

yy	101	gmgmguguproasp	leuasp	prop	roarg	gug	lury	arg	114
Db	2513	CAGGAGGAGCCAG	AGCTAG	ACCCAC	CCCGGGA	GAGAGT	ACAGA		2554

RESULT	7	-	
LOCUS	AX477390		
DEFINITION	AX477390	3001 bp	DNA
Sequence	4 from Patent WO024475	linear	PAT 12-AUG-2002

ACCESSION	AX477390
VERSION	AX477390.1
KEYWORDS	GI:22216619
SOURCE	Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

AUTHORS Chaimley, F., Moss, F. and Meeuën, M.
TITLE Compositions and methods for diagnosing or treating psoriasis
JOURNAL Patent: WO 024375-A 4 06-JUN-2002;
Celltech R & D, Inc. (US)

```
location/Qualifiers
source
1. 3001
/organism="Homo sapiens"
/mol type="unassigned DNA"
```

Alignment Scores:

Score:	692.00	Matches:	114
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

DB: 6 Gaps: US-09-994-365-3 (1-114) x AX47390 (1-3001)

[illegible][illegible]

QY 41 ASPProProProThrArgProSerArgProTrpArgSplenuProGluThrGlyValTrp 60
 Db 2337 GATCCTCCGCGCTAACCGCCCGAGTCGTCCTCGAGAGACCTGCTGTAACCTGAGTCTGG 2396

QY 61 FROProGIuNProProArgThrasPProProGIuNProBroAsPProAsPProTTPPro 80
 |||||
 Db 2397 CCCCCTGAACGGCCTTGAACGGATCTCTCAACCTCCCCGGCGCTGACGACCTTTGGCGC 2456

QY	81	AAGLYP	ProGlnProGluAsnProTyrProProAlaProGluValAspAsnArgPro	100
Db	2457	GCAAGAACCCACGCCCTGGCTTCCTGCCTCGAGGTGGACAACCGACT		2516

[illegible]

RESULT 8	BD095297	25235 bp	DNA	linear	PAT 27-AUG-2002	
LOCUS	BD095297	25235 bp	DNA	linear	PAT 27-AUG-2002	
DEFINITION	The method of testing for psoriasis vulgaris.					
ACCESSION	BD095297					
VERSION	BD095297.1	GI:22640885				
KEYWORDS	MO 0142458-A/2.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	1 (bases 1 to 25235)					
TITLE	Inoko, H. and Tamiya, G.					
JOURNAL	The method of testing for psoriasis vulgaris					
	Patent: WO 0142458-A 2 14-JUN-2001;					
	HIDETOSHI INOKO, GEN TAMIYA					
COMMENT	OS Homo sapiens (human)					
	PN WO 0142458-A/2					
	PD 14-JUN-2001					
	PF 06-DEC-2000 WO 2000JP008624					
	PR 06-DEC-1999 JP 99P 346867					
	PI HIDETOSHI INOKO, GEN TAMIYA					
	PC C12N15/12, C12Q1/68					
	CC The method of testing for psoriasis vulgaris					
	FH Key					
	Location/Qualifiers					
	FT exon (1).. (420)					
	FT exon (1282).. (1405)					
	FT exon (1602).. (1702)					
	FT exon (1602).. (1631)					
	FT exon (2352).. (2364)					
	FT exon (6287).. (6509)					
	FT exon (10417).. (10493)					
	FT exon (14244).. (14407)					
	FT exon (14244).. (14344)					
	FT exon (25190).. (25235).					
FEATURES	Location/Qualifiers					
source	1..25235					
	/organism="Homo sapiens"					
	/mol_type="genomic DNA"					
	/db_xref="taxon:9606"					
ORIGIN						
Alignment Scores:						
Pred. No.:	6.14e-19	Length:	25235			
Score:	692.00	Matches:	114			
Percent Similarity:	100.00%	Conservative:	0			
Best local Similarity:	100.00%	Mismatches:	0			
Query Match:	100.00%	Indels:	0			
DB:	6	Gaps:	0			
US-09-994-365-3 (1-114) x BD095297 (1-25235)						
QY	1	SergluglYHt	ProSeRHi	ProProAla	AGluAAspAGluGluAlaAGlySerProThr 20	
Db	1766	AGCGAGGCGCACCTCTC	ACCCACCCGCAAGAGAC	CGAGAGGCGAGGCTCCCAACA	182535	
QY	21	LeuProGlnGlu	ProProVal	ProGlyAsp	ProTrpProGlyAlaProLeuPheGlu 40	
Db	1826	TTGGCTCAGGGGCCCGCC	CGGTCGACCTTGCCAGAGGGGAC	CCCCCTCTTTGAA	18855	
QY	41	AspProP	ProP	ProThrAsp	ProSerArgProTrpArgAspLeuProGluThrGlyValTrp 60	
Db	1886	GATCTCCGCTACCCGCGCC	CGACAGTCGCTCCGAGAGAC	CTGCTCGAATCGGAGTCTGG	194545	
QY	61	ProProGlu	ProProArg	ThrAsp	ProProGlnInP	ProProArgProAspAspProTrpPro 80
Db	1946	CCCCCTGAACCGCTCAGAAC	CGGATCTCTCAACTCCCGGCGCT	GCAGCAGCCCTTGGCGG	200505	
QY	81	AlaGlyProGln	ProProGlu	AsnProTrp	ProProAlaProGluValAspAsnArgPro 100	
Db	2006	GCAGAGCCCAAGCCCAAGAAA	ACCCCTCGCTCTGCGCCCTGAGGTG	AGAACCGACT	206555	
QY	101	GlnGluGlu	ProProAsp	LeuAsp	ProProArgGluTrpArg 114	

Dn		2066 CAGGAGGACCGAACCTTAGACCACCCCGGGAGAATACACA	2107
RESULT_9			
AB088114/c			
LOCUS	AB088114	30911 bp	DNA linear PRI 08-JAN-2003
DEFINITION	Homo sapiens STG, S, SPR1, SEEK1 genes.		
ACCESSION	AB088114		
VERSION	AB088114.1	GI:27544424	
KEYWORDS	.		
ORGANISM	Homo sapiens (human)		
SOURCE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	1		
AUTHORS	Shima,T., Ota,M., Katsuyama,Y., Hashimoto,N. and Inoko,H. Genome diversity in HLA: A new strategy for detection of genetic polymorphisms in expressed genes within the HLA class III and class I regions		
TITLE	Unpublished		
JOURNAL	2 (bases 1 to 30911) Shima,T.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (08-JUL-2002) Takaishi Shima, Tokai University School of Medicine, Molecular Life Science 2; Bohseidai, Isehara, Kanagawa		
TITLE	259-1193 Japan (E-mail:tchinn@tsl.tcc.u-tokai.ac.jp, Tel:81-463-93-1121, Fax:81-463-94-8884)		
JOURNAL	Location/Qualifiers		
FEATURES	1..30911		
source	/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="6" /map="p21.31" /cell_line="LKT3" /cell_type="B cell" 1317..2383 /number=2 complement(join(1473..2383,2581..2647)) /gene="STG" complement(join(1473..2383,2581..2647)) /gene="STG"		
exon	/codon_start=1 /product="hypothetical protein" /protein_id="BA054947.1" /db_xref="GI:27544425"		
CDS	translation="MOGRVAGSCAPLGILLVCLHLPGLPARSIGVEEKYSQNLGTNMLPOLGSGTNGNSSEHPDALDPSNDLARVLKLSYPAADGPDPAGSAVORMPSPSMGLPRAMDWPEDPPQQWMAAAAEDELREALPEBSYLSSAALAAGSGPLGESPDNTGLSPKSALIHODESRRLPRSNSLGAAGKITLSORPVSLTHRVLEPDMKLTVSNRGGDGPOGWGTIRPMPIHEBGIMGINNOPGTSWGNTINYPGSWGNIIRYPGSWGNIINRYPCGSWGNIHLVYGINNPPPGLRPGLRPGSSWNIPAGFPMPSPRLQMG"		
exon	2581..2647 /number=1 4938..4983 /number=1 5185..7618 /number=2 complement(join(6114..7618,10423..10459)) /gene="S"		
exon	- /codon_start=1 /product="modified desmosin expressed in non-cornified epidermis"		
exon	/protein_id="BA054948.1" /db_xref="GI:27544426"		
exon	/translation="MMALLLAGLLPGLTAKEISGTESDPECKDRITRSNPDECITKGKDSSGFSSVSASSSSGISISSARSGSGSSSGSSSIJAOGASAFRGIVGYGVSYSDSGSSIQAGASSQSOLSSSHSGSSHSSSSSSSQFSSSFQVGNGMALPTMDNYRGTILGNLSPGOSSSSOTSGSVSSGOSVNORCSADIIDPSCGGPIVSHSGRIIHSHSVSGCGRPYYVVVDQTSGSARPYVOCPGCCNGGIRPKGPCPIRSSGKY YGGIEVVGSSDSLTFGMITYSKKTIYPGVIFTKENVPKSPGVPSFAAGPIISEGKY		
gene			
CDS			

```

FSSNPITPQGAASATAFOFVGTGVOLCGGSGTGKPCSPSSSRVPSSSISSS
GSPHPCGASQSPSPGCTGSSSSSSSSGKIILOPCGSKSSSGHPCMVYSIT
LTGGPDGPHDPGAKAPCGSSSAGKIPGSIINDILAQVPELPQADPEVFLPQSE
LTDSP"
exon      10423..10521
           /number=1
exon      15765..15928
           /number=2
exon      19676..19752
           /number=3
exon      27641..28413
           /number=2
           complement (join(28058..28413,29079..29133))
gene       /gene="SPR1"
           complement (join(28058..28413,29079..29133))
           /gene="SPR1"
           /codon_start=1
           /product="hypothetical protein"
           /protein_id="BAC54949.1"
           /db_xref="GI:27544427"
           /translation="MILNWKILGIVLCLHTRGISGSEGHSPHPADREAGSPTLP
           QGPVDPDMPGAPLPFEDPPPTPSRPMDDLPTGVWPPPEPPTDPPQDPDDPMP
           AGQPENMPMPAPBEVNRQGEEDLDPPREBYR"
exon      28537..28566
           /number=4
exon      28763..28886
           /number=5
           join(28864..28886,29748..30039)
gene       /gene="SEEK1"
           join(28864..28886,29748..30039)
           /gene="SEEK1"
           /codon_start=1
           /product="hypothetical protein"
           /protein_id="BAC54950.1"
           /db_xref="GI:27544428"
           /translation="MEPANHFMAQDIQAMISKEFHIAATODCRKROEDIVSS
           HPEIFASVLPMAPEARLQOPPLPPPSGIHLSAKRTLLPTLLSPSPSHSFFGLSS
           LI"
exon      29079..29448
           /gene="SEEK1"
           /number=1
exon      29748..30167
           /number=6

ORIGIN
Alignment Scores:
Pred. No.:      7,11e-19      Length:      30911
Score:          692.00        Matches:      114
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             9            Gaps:        0

US-09-994-365-3 (1-114) x AB088114 (1-30911)
QY      1  SerGIUGLVIHISProSerHiSPProRoAlaGIuAspAroGIuGLuAlaGIuSerProThr 20
Db      28402 AGCGAGGGCCACCCCTCTCAACCAACCGCAGAGACCGAAGAGAGAGCGAGGCTCCCAACA 28343
QY      21  LeuProGIuNGIYProProValProGIYAspProTIPProGIYAlaProProLeuPheGlu 40
Db      28342 TTGCTCTCAGGGCCCCCAGTCCCGGTGACCTTGCGCAGGGGCAACCCCTCTCTTTGAA 28283
QY      41  AspProProProThrArgProSerArgProTIPArgAspLeuProGIuThrGIYAlaTTP 60
Db      28282 GATCCCTCCGCTTACCGGCCAGTCTGCTCGAGAGAGACCTGCTGAACCTGGAAGTCTGG 28223
QY      61  ProProGIuProProRoArgThArgProProRoGIuInProProArgProAspAspProTIPPro 80
Db      28222 CCCCCGAAACCGGCTTGAACGAGTCTCTCTCAACCTCCCGGCTTACGACCTCTTGCGCG 28163
QY      81  AlaGIYProGIuProProRoArgThArgProProRoGIuInProProAlaProGIuValAspAsnArgPro 100

```

```

Db      28162 GCAGAGACCCAGGCCCCAGAAACCCCTGGGCTCTGCCCCCTGAGGTGACAAACGACCT 28103
QY      101  GInGIuGIuProAspLeuAspProProRoArgGIuGIuTyrArg 114
Db      28102 CAGAGAGAGCCAGACCTAGACCAACCCCGGAGAGAGACAGA 28061

RESULT 10
AB023060
LOCUS      39196 bp      DNA      linear      PRI 20-NOV-1999
DEFINITION Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region,
            clone:TY1C2, complete sequence.
ACCESSION  AB023060
VERSION    AB023060.1  GI:5672629
KEYWORDS   HTG.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  Shihina,T., Tamiya,G., Oka,A., Takishima,N., Yamagata,T.,
            Kikkawa,E., Iwata,K., Tomizawa,M., Okuaki,N., Kuwano,Y.,
            Watanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,
            Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,
            Bahram,S. and Inoko,H.
            Molecular dynamics of MHC genes is unraveled by sequence analysis of
            the 1,796,938-bp HLA class I region
            Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)
JOURNAL   MEDLINE
PUBMED    20027539
TITLES    10557312
REFERENCE 2 (bases 1 to 39196)
AUTHORS   Shihina,T. and Takishima,N.
TITLES    Direct Submission
JOURNAL   Submitted (29-JAN-1999) Takeshi Shihina, Tokai University School of
            Medicine, Department of Molecular Life Science 2, Bohseidai,
            Isehara, Kanagawa 259-1193, Japan
            E-mail:tsuhina@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121,
            Fax:81-463-94-8884)
FEATURES
source
1..39196
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
/clone="TY1C2"
/cell_line="BOLETH"
/tissue_type="B cell line"

Alignment Scores:
Pred. No.:      8.44e-19      Length:      39196
Score:          692.00        Matches:      114
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             9            Gaps:        0

US-09-994-365-3 (1-114) x AB023060 (1-39196)
QY      1  SerGIUGLVIHISProSerHiSPProRoAlaGIuAspAroGIuGLuAlaGIuSerProThr 20
Db      10646 AGCGAGGGCCACCCCTCTCAACCAACCGCAGAGACCGAAGAGAGAGCGAGGCTCCCAACA 10705
QY      21  LeuProGIuNGIYProProValProGIYAspProTIPProGIYAlaProProLeuPheGlu 40
Db      10706 TTGCTCTCAGGGCCCCCAGTCCCGGTGACCTTGCGCAGGGGCAACCCCTCTCTTTGAA 10765
QY      41  AspProProProThrArgProSerArgProTIPArgAspLeuProGIuThrGIYAlaTTP 60
Db      10766 GATCCCTCCGCTTACCGGCCAGTCTGCTCGAGAGACCTGCTGAACCTGGAAGTCTGG 10825
QY      61  ProProGIuProProRoArgThArgProProRoGIuInProProArgProAspAspProTIPPro 80

```



```
repeat_region      24066.24312
                    /rpt_family="Alu"
repeat_region      complement(24673).24731
                    /rpt_family="Alu"
repeat_region      complement(24760).25051
                    /rpt_family="Alu"
repeat_region      complement(27927).28526
                    /rpt_family="Alu"
repeat_region      complement(28990).29259
                    /rpt_family="Alu"
repeat_region      complement(29340).29635
                    /rpt_family="Alu"
repeat_region      29889.30145
                    /rpt_family="Alu"
repeat_region      30250.30564
                    /rpt_family="Alu"
repeat_region      30791.31421
                    /rpt_family="Alu"
repeat_region      complement(32533).33421
                    /rpt_family="Alu"
repeat_region      complement(33782).34080
                    /rpt_family="Alu"
repeat_region      34426.35134
                    /rpt_family="Alu"
repeat_region      complement(35292).35444
                    /rpt_family="Alu"
repeat_region      complement(37575).37780
                    /rpt_family="Alu"
repeat_region      complement(40336).40717
                    /rpt_family="Alu"
```

Pred. No.:	8.7e-19	Length:	40878
Score:	692.00	Matches:	114
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

QY	1	SeGInGInIyHISProSeRTHISProProlAGInAAsPAGInIyInIaGInySeRProTr	20
Db	27100	AGCGAGGAGCCACCCCTCTCACCCACCCGACAGAGGACCGAGAGGACGAGGACGCTCCCAACA	27159
QY	21	LeuPProGInGInIyProProValProGIyAspProTIPProGIyAlaProPLeuPheGIn	40
Db	27160	TTGGCTCAGGAGCCCCCGAGTCCCGGAGACCTTGGCAGGGGACACCCCTCTTTTGA	27219
QY	41	AsPProPProPothuArgProSeRAsPProTIPArgAsPLeuProGInuhrgIyAlTIP	60
Db	27220	GATCTCTCGGCTACCCGCCCAAGTCGTCCCTGGAGAGACCTGCTAAACTGGAGTCTGG	27279
QY	61	ProPProGInuPProPothuArgThAsPProProGInuPProPProArgProAspPProTIPPro	80
Db	27280	CCCCCTTAACCGCTTAACAGGAGCTCTCTCAACTCTCCCGGCTTAACGACCTTGTGGCG	27339
QY	81	AlaGInyProGInuPProPProGInuAsnPProTIPProProAlaProGInuValAspAsnArgPro	100
Db	27340	GCAAGAACCCGAGCCGCCCAAGAAAAACCTCTGGCGTCTCTGCCCCCTGAGGTGACCAACGACCT	27399
QY	101	GInGInuGInuPProAsPLeuAsPProPProPothuArgInIyTyrArg	114
Db	27400	CAGAGAGAGCCAGACTTAAGACCAACCCCGGAGAGAGTACAGA	27441

RESULT	12				
AX522117					
LOCUS	AX522117	55050 bp	DNA	linear	PAT 24-OCT-2002
DEFINITION	Sequence 4 from Patent WO02064831.				
ACCESSION	AX522117				
VERSION	AX522117.1	GI:24411002			
KEYWORDS	.				

```

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
AUTHORS     Lench,N.J., Allen,M.J. and Nicholls,R.K.
TITLE        Test and model for inflammatory disease
JOURNAL      Patent: WO 02064831-A 4 22-AUG-2002;
            Oxagen limited (GB)

FEATURES
SOURCE      1..55050
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

ORIGIN

```

Alignment Scores:	
Pred. No.:	1.08e-18
Score:	692.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	6
Gaps:	0
Length:	55050
Matches:	114
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-994-365-3 (1-114) X AX522117 (1-55050)

QY	1	SerGluGluYhiAproSerhiAproProAlaGluAAspArgGluGluAlaGlySerProThr	20
Db	27111	AGGAGGGCCACCCCTCTACCCACCCGAGAGAACGAGAGGAGCAGGCTCCCCACAC	27170
QY	21	LeuProGluGluYProProValProGluAAspProTrpProGluValAProProLeuPheGlu	40
Db	27171	TTGGCTCAGGGCCCCCAGTCCCGGTGACCTTGGCCAGGGGACCCCTCTCTTTGAA	27230
QY	41	AspProProProThrArgProSerArgProTrpArgAspLeuProGluThrGlyValTrp	60
Db	27231	GATCTCCGGCTACCGGCCCAAGTCGTCCCTGAGAGACCTGCTGAACATGSAATCTCGG	27290
QY	61	ProProGluProProAlaArgThrAspProProGluProProArgProAspAspProTrpPro	80
Db	27291	CCCCCTGAACCGGCTCTGAAACGATCTCTCTCAACCTCCCGGCGTCGACGACCTTTGGCGG	27350
QY	81	AlaGlyProGluInProProGluAAspProTrpProProAlaProGluValAspAsnArgPro	100
Db	27351	GCAAGACCCCAAGCCCCCAGAAAAACCCCTGACCTCTGAGAGTGAACACCGACT	27410
QY	101	GlnGluGluProAspLeuAspProProArgGluGluTrpArg	114
Db	27411	CAGAGAGACCAAGACTGAGCCACCCCGGAGAAATACAGA	27452

RESULT 13	AL662867	70288 bp	DNA	linear	PRI 24-APR-2002
LOCUS	AL662867/c				
DEFINITION	AL662867				
	Human DNA sequence from clone XKBac-34D1 on chromosome 6, complete sequence.				
ACCESSION	AL662867				
VERSION	AL662867.5	GI:20068664			
KEYWORDS	HTG.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1				
AUTHORS	Sycamore, N.				
TITLE	Direct Submission				
JOURNAL	Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton,				

Cambridge, CB10 1SA, UK. E-mail enquiries: clonerequest@sanger.ac.uk
humuery@sanger.ac.uk. Clone requests: clonerequest@sanger.ac.uk
On Apr 7, 2002 this sequence version replaced 91.19309550.
During sequence assembly data is compared from overlapping clones
Where differences are found these are annotated as variations
variation with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SwissProt; Tr, TrEMBL; Wp, WormPeP; information on the WormPeP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep XXbac-34D1 is from a CHORI-502 human bac - COX cell line library VECTOR: PFARAC2.1

This sequence was generated from part of bacterial clone contigs constructed by the MHC Haplotype Consortium and collaborators. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6/MHC>.

FEATURES

source

1. 70288
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/clone="XXbac-34D1"
/clone_1lb="CHORI-502"

ORIGIN

Alignment Scores:

Pred. No.:	Length:	70288
Score:	692.00	Matches: 114
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	9	Gaps: 0

US-09-994-365-3 (1-114) x AL662867 (1-70288)

QY 1 SerGUGUyHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThr 20
Db 67711 AGGAGGGGACACCCCTCTCAACCCGACAGAGACCGAGAGGAGGAGGCTCCCAACA 67652
QY 21 LeuProGlnGlyProProValProGlyAspProTrpProGlyAlaProProLeuPheGlu 40
Db 67651 TTGGCTCAGGACCCCGACGTCCTCCGAGTGGCCAGGGGACCCCTCTTGGAA 67592
QY 41 AspProProThrArgProSerArgProTrpArgAspLeuProGluThrGlyValTrp 60
Db 67591 GATCCTCCGCTACCGCCGACGTCCTGAGAGACCTGCTGAACTGGAAGTCTGG 67532
QY 61 ProProGluProProArgThrAspProProGlnProProAlaArgProAspProTrpPro 80
Db 67531 CCCCTGAAACCGCTGAAAGAGATCTCTCAACCTCCCGGCTGACGACCTTGGCCG 67472
QY 81 AlaGlyProGlnProProGluAsnProTrpProProAlaProGluValAspAsnArgPro 100
Db 67471 GCGAGACCCAGCCCGCAAAACCTCGGCTCTCTGCGCTGAGGAGCAACCGACCT 67412
QY 101 GlnGluGlnProAspLeuAspProProArgGluGluValTrpArg 114
Db 67411 CAGAGAGAGCCACCACTAGACCCCGGGAAGAGTACAGA 67370

RESULT 14
AP000510
LOCUS AP000510 99999 bp DNA linear PRI 22-AUG-2001
DEFINITION Homo sapiens genomic DNA, chromosome 6p21.3, HLA Class I region,
section 9/20.
ACCESSION AP000510 BA000025
VERSION AP000510.2 GI:7380878
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 Shima, S., Tamiya, G., Oka, A. and Inoko, H.
Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region

JOURNAL

Published Only in Databases (1999)

REFERENCE

2 (bases 1 to 99999)

AUTHORS

Hirakawa, M., Yamaguchi, H., Imai, K. and Shimada, J.

TITLE

Submitted (21-SEP-1999) Mika Hirakawa, Japan Science and Technology

JOURNAL

Corporation (JST), Advanced Databases Department; 5-3, Yodobancho,
Chiyoda-ku, Tokyo 102-0081, Japan (E-mail: mikae@okyo.jst.go.jp,
URL: <http://www-alle.tokyo.jst.go.jp/>, Tel: 81-3-5214-8491,
Fax: 81-3-5214-8470)

COMMENT

On Mar 31, 2000 this sequence version replaced gi:5926697.
This sequence is conducted by Tokai University as a JST sequencing
Team.

Principal Investigator: Hidetoshi Inoko Ph.D
Phone: +81-463-93-1121, Fax: +81-463-94-8884,
The sequence is submitted by Human Genome Sequencing in ALIS
project of JST

Japan Science and Technology Corporation (JST)
5-3, Yodobancho, Chiyoda-ku, Tokyo, 102-0081 Japan
For further information about this sequences, please visit our
sequence archive Web site (<http://www-alle.tokyo.jst.go.jp/HGS/top.html>) or send email to webmaster@www-alle.tokyo.jst.go.jp

Sequence updated (28-Mar-2000).
Location/Qualifiers

FEATURES

source

1. 99999
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
/map="6p21.3"
2016. .2435
/gene="SBEK1"
2016. .2435
/gene="SBEK1"
/number=6
/complement (join(2144. .2435,3297. .3319))
/gene="SBEK1"
complement (join(2144. .2435,3297. .3319))
/gene="SBEK1"
/codon_start=1
/protein_id="BAB63314.1"
/db_xref="GI:15277221"
/translation="MRPNHFWHAGDLOMISKFFLAATODCRKGRTOEDILVPS
HPELFASVPMAPBEAARLQOPPLPPSGIHLSARTLAPTLVSSPPSHSPGLSS
LI"

exon

gene

CDs

exon

gene

CDs

exon

gene

exon

exon

```

gene      /number=2
          12432..16422
          /gene="SBEK1"
exon      12432..12508
          /gene="SBEK1"
          /number=3
exon      16259..16422
          /gene="SBEK1"
          /number=2
gene      21667..27003
          /gene="S"
          21667..21765
          /gene="S"
          /number=1
          join(21729..21765,24570..26074)
          /gene="S"
          /codon_start=1
          /protein_id="BAB63316.1"
          /db_xref="GI:15277223"
          /translation="MMALLAGLLPGLTAKISGTPSPDKDPTRTITSPNDPCLTGKG
          DSGGFSYSGSSSSSGSISAPSSGSSSSGSSSTAOAGSAGSPKPGTGVDSVYS
          SSGSSLIQGAAGSSQUGSSSSSHGSSGSSSHSSSSSTQFSSSSSTQVNGAHL
          PTMDSYRGILNPSQPGQSSSSQTSVSSSSGQSVSSNQPCSDIPDSFCGPIVS
          HSGPYIPSSSHSVGQGPVVVVVDHSGSAPGVQGPCCNGALPGKPCPITSVKX
          YGAEVVGSSDSYLVGWTYSKGIYPVGYFTKEMPKGSPGVPSFAAGPPISEGY
          FSNRPITPQSAASAIAPQVGTGVOLCGGSGTSGKPCSPSSSSSSSSSSSS
          GSPYHPCGASGSCPCSPRTGSPSSSSSSSGKTIILQPCGSKSSSGHPGMSVSLT
          LTGPDGSPHPDPSAGAKPCGSSSAGKIPKRSIRDLIAQVPLGPQLADPRVLPQGE
          LIDSP"
exon      24570..27003
          /gene="S"
          /number=2
          26711..26940
          /gene="S"
          /note="RH17634;The location is between each flanking site
          of PCR primers."
          /db_xref="GDB:4572035"
          27205..27250
          /gene="SBEK1"
          27205..27250
          /gene="SBEK1"
          /number=1
exon      exon
          /number=1
ORIGIN
Alignment Scores:
Pred. No.: 1.66e-18      Length: 99999
Score: 692.00      Matches: 114
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 9      Gaps: 0
US-09-994-365-3 (1-114) x AD000510 (1-99999)
QY      1 SerGluGlyHisProSerHisProProAlaGluAspArgGluGluValIserProThr 20
Db      3781 AGCGAGGGCCACCCCTCTCACCCGACGAGAGACCGAGAGGAGCGAGGCTCCCAACA 3840
QY      21 LeuProGlnGlyProProValProGlyAspProTrpProGlyAlaProProLeuPheGlu 40
Db      3841 TTGGCTCAGGGCCCCCAGTCCCGGTGACCTTGGCGCAGGGGCACCCCCTCTTTGAA 3900
QY      41 AspProProProThrArgProSerArgProTrpArgAspLeuProGluThnGlyValTrrp 60
Db      3901 GATCTCCGGCTACCGCGCCAGTGTCTCTGGAGAGACTGCTGAAACTGGAGTCTGG 3960
QY      61 ProProGluProProArgTrpAspProProGlnInProProAlaArgProAspAspProTrpPro 80
Db      3961 CCCCTGAAACCGCTAGAGAGGATCCTCTCAACTCCCGGCGCTGACGACCTTTGGCGG 4020
QY      81 AlaGlyProGlnInProProGluAsnProTrpProProAlaProGluValAspAsnArgPro 100
Db      4021 GCAAGACCCCGACCCCGAAGAAACCCCTGGCTCTGCTGCGCTGAGTGAACACCGACT 4080

```

```

QY      101 GlnGluGlyProAspLeuAspProProArgGluGluTyrArg 114
Db      4081 CAGAGAGCCGACCTAGACCCACCCCGGAGAGAGTACAGA 4122
RESULT 15
AL773544/c
LOCUS
DEFINITION
Human DNA sequence from clone DA0B-18511 on chromosome 6, complete
sequence.
ACCESSION
AL773544
VERSION
AL773544.5
KEYWORDS
HTG.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 113388)
Direct Submission
Submitted (21-OCT-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk
On Oct 21, 2003 this sequence version replaced gi:22735515.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
-----
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WormPeP; Information
on the WormPeP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence
was generated from part of bacterial clone contigs constructed by
the MHC Haplotype Consortium and collaborators. Further information
can be found at
http://www.sanger.ac.uk/HGP/Chr6/MHC
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
DA0B-18511 is from a DNA-arts OBL human bac library VECTOR.
pbclOBAC11.
FEATURES
source
Location/Qualifiers
1..113388
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/clone="DA0B-18511"
/clone_1lb="DNA-arts-BAC.1-OB1.1"
ORIGIN
Alignment Scores:
Pred. No.: 1.82e-18      Length: 113388
Score: 692.00      Matches: 114
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 9      Gaps: 0

```

US-09-994-365-3 (1-114) x AL773544 (1-113388)

```

QY      1 SerGluGlyHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThr 20
      |||
Db      60131 AGCGAGGGCCACCCCTCTCAACCCCGCAGAGGACCGAGAGGAGGCGCTCCCAACA 60072
QY      21 LeuProGlnGlyProProValProGlyAspProTyrProGlyAlaProProLeuPheGlu 40
      |||
Db      60071 TTGCCTCAGGGGCCCCCAGTCCCGGTGACCTTGCCAGGGGCACCCCCTCTTTGAA 60012
QY      41 AspProProProThrArgProSerArgProTyrPheAspLeuProGluThrGlyValTyr 60
      |||
Db      60011 GATCCTCCGGCTACCCCGCCAGTCGTCCCTGGAGAGACCTGCCTGAACCTGAGTCTGG 59952
QY      61 ProProGluProProArgThrAspProProGlnProProArgProAspAspProTyrPro 80
      |||
Db      59951 CCCCCTGAAACCGCTTACAGACGATCTCTCAACCTCCCGGCTGACGACCTTGCGCG 59892
QY      81 AlaGlyProGlnProProGluAsnProTyrProProAlaProGluValAspAsnArgPro 100
      |||
Db      59891 GCAGGAGCCCGAGCCCGCAAAACCCCTGGGCTCTGCCCCCTGAGGTGACCAACGACCT 59832
QY      101 GlnGluGluProAspLeuAspProProArgGluGluTyrArg 114
      |||
Db      59831 CAGGAGGAGCCAGACTTACAGACCCCGGAGAGGTACAGA 59790

```

Search completed: January 11, 2005, 13:59:25
 Job time : 3163.24 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 11, 2005, 10:41:32 ; Search time 3693.76 Seconds
(without alignments)
1741.152 Million cell updates/sec

Title: US-09-994-365-2
Perfect score: 808
Sequence: 1 MILMWKLGLVLCILHTRGI.....EVDNRQBPEDLDPPREYR 136

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ .p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO.spool.h/US09994365/runat_10012005_172231_6821/app_query.fasta_1.590
-DB=GenBml -QFMT=fastap -SUFRTX=p2n.rge -MINMATCH=0.1 -LOOPT=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NORM=ext -HEADING=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09994365_QCGN_1_1_3851@runat_10012005_172231_6821 -NCP=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenBml:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	808	100.0	891	6	AX477387 Sequence
2	808	100.0	1143	6	CQ722444 Sequence
3	808	100.0	1143	9	AB031480 Homo sapi
4	808	100.0	1185	9	AF484420 Homo sapi

5	808	100.0	1473	6	AX406002	AX406002 Sequence
6	712	88.1	2997	6	AX477396	AX477396 Sequence
7	712	88.1	3001	6	AX477390	AX477390 Sequence
8	712	88.1	25235	6	BD095297	BD095297 The metho
9	712	88.1	30911	9	AB088114	AB088114 Homo sapi
10	712	88.1	39196	9	AB023060	AB023060 Homo sapi
11	712	88.1	40878	9	AC004195	AC004195 Homo sapi
12	712	88.1	55050	6	AX522117	AX522117 Sequence
13	712	88.1	70288	9	AL662867	AL662867 Human DNA
14	712	88.1	99999	9	AP000510	AP000510 Homo sapi
15	712	88.1	113388	9	AL773544	AL773544 Human DNA
16	712	88.1	135336	9	BX927139	BX927139 Human DNA
17	702	86.9	204298	9	AL662844	AL662844 Human DNA
18	686	84.9	175689	9	AC148703	AC148703 Macaca mu
19	682	84.4	300050	9	AB100083	AB100083 Pan trogl
20	672	83.2	200068	9	AC148691	AC148691 Macaca mu
21	617	76.8	383	4	AF484422	AF484422 Sus scrof
22	588	72.8	154749	4	AB113354	AB113354 Sus scrof
23	573.5	71.0	809	10	AF484421	AF484421 Mus muscu
24	536.5	66.4	773	10	AF159091	AF159091 Mus muscu
25	522	64.6	349571	10	BX883047	BX883047 Rattus no
26	516.5	63.9	1377	10	AF159090	AF159090 Mus muscu
27	516.5	63.9	159179	10	MMHC322F16	MMHC322F16
28	516.5	63.9	226594	10	AC087216	AC087216 Mus muscu
29	449	55.6	349980	6	AX344554	AX344554 Sequence
30	304.5	37.7	248	6	AR418279	AR418279 Sequence
31	304.5	37.7	248	6	AX978973	AX978973 Sequence
32	304.5	37.7	248	6	BD113832	BD113832 EST and e
33	258	31.9	388	9	HS114A35	HS114A35 Human H1A c
34	212.5	26.3	164520	2	AC020738	AC020738 Homo sapi
35	210	26.0	247221	2	BX470211	BX470211 Dario rer
36	208	25.7	185549	2	BX927317	BX927317 Dario rer
37	207.5	25.7	152340	2	CR396595	CR396595 Dario rer
38	206.5	25.6	91040	5	BX248094	BX248094 Zebrafish
39	206.5	25.6	166514	5	BX469924	BX469924 Zebrafish
40	205	25.4	177205	2	CR376782	CR376782 Dario rer
41	205	25.4	185411	2	BX548008	BX548008 Dario rer
42	205	25.4	225024	2	CR394539	CR394539 Dario rer
43	204.5	25.3	155657	2	BX469901	BX469901 Dario rer
44	204	25.2	242992	2	BX569798	BX569798 Dario rer
45	203.5	25.2	161366	5	BX005382	BX005382 Zebrafish

ALIGNMENTS

RESULT 1	AX477387	891 bp	DNA	linear	PAT 12-AUG-2002
LOCUS	AX477387				
DEFINITION	Sequence 1 from Patent WO0244375.				
ACCESSION	AX477387				
VERSION	AX477387.1	GI:22216617			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	1				
AUTHORS	Charnley, P., Moss, P. and Mceuen, M.				
TITLE	Compositions and methods for diagnosing or treating psoriasis				
JOURNAL	Patent: WO 0244375-A 1 06-JUN-2002;				
CELLTECH R & D, Inc. (US)					
FEATURES	Location/Qualifiers				
source	1..891				
	/organism="Homo sapiens"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
	64..474				
	/note="unnamed protein product"				
	/codon_start=1				
	/protein_id="CAD43680.1"				
	/db_xref="GI:22216618"				
	/translation="MILMWKLGLVLCILHTRGISGSEGHSHPPADREASPTLP				
	/translaton="MILMWKLGLVLCILHTRGISGSEGHSHPPADREASPTLP				
	QGPVPDGPWGAAPLPEEDPPRSPRPMRDLPETGVWPEPEPRTPDPQPPRPDDPWP				

/gene="SPR1"
/codon_start=1
/protein_id="BA08131.1"
/db_xref="GI:6539434"
/translation="MTLNMKILGLVLCIHTRGISGSEGHSPHPADREAGSPITP
QGPVGDPPWPGAPPLFEDPPPTPSRPMRDLEPTGWPPEPPRTDPPQPRDDPWP
AGQPPENPWPAPAEVDNRPQEEPDIDPREYR"

ORIGIN

Alignment Scores:

Pred. No.:	2.49e-24	Length:	1143
Score:	808.00	Matches:	136
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-994-365-2 (1-136) x AB031480 (1-1143)

QY 1 MetIleuAsnTrpLysLeuLeuGlylleuValIleuCySteuHsThrArgGlylle 20
DB 316 ATGATCTCACTGAGAGCTCTGGGATCTGCTCTTGCTCGACACCAAGGATC 375
QY 21 SerGlySerGlyGlyHisProSerHisProProAlaGluAspArgGluGluAglYser 40
DB 376 TCAGGCGAGGAGGCGACCCCTCTCACCCCGCAGAGGACCGAGAGGAGGCGCTCC 435
QY 41 ProThreuProGlnGlyProProValProGlyAspProTrpProGlyAlaProProLeu 60
DB 436 CCAACATTTGCTCAGAGGCCCCCGGATCCCGGTGACCTTGCGCAGAGGACCCCCCTCTC 495
QY 61 PheGluAspProProTrpThrArgProSerArgProTrpArgAspLeuProGluThrGly 80
DB 496 TTGGAAGATCTCTCGCTTACCCGCCCAAGTCGTCTCTGAGAGACTGCTGAAACTGGA 555
QY 81 ValTrpProProGlnProProValProGlyAspProProGlnProProArgProAspAspPro 100
DB 556 GTCTGGCCCCCTGAAACCGCTAGAACGATCTCTCAACCTCCCGGCTGACGACCT 615
QY 101 TrpProAlaGlyProGlnProProGluAsnProTrpProProAlaProGluValAspAsn 120
DB 616 TGGCCGCGAGAGACCCGAGCCCGGAAACCCCTGCGCTCTGCGCTGAGGTGACAC 675
QY 121 ArgProGlnGluGluProAspLeuAspProProArgGluGluYrArg 136
DB 676 CGACCTCAGAGAGACCACTAGACCCACCCCGGAAAGTACAGA 723

RESULT 4
AF484420 1185 bp mRNA linear PRI 02-MAR-2003
LOCUS Homo sapiens psoriasis susceptibility 1 candidate 2 (PSORS1C2)
DEFINITION
AF484420
VERSION AF484420.1 GI:28628834
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Holm,S.J., O'Brien,K.P., Carlen,L. and Stahle-Backdahl,M.
TITLE The PSORS1C1 and PSORS1C2 genes in 6p21.3 associate strongly with
psoriasis in the Swedish population
JOURNAL Unpublished
2 (bases 1 to 1185)
REFERENCE
AUTHORS Holm,S.J., O'Brien,K.P., Carlen,L. and Stahle-Backdahl,M.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-2002) Dermatology, Karolinska Institute, L8:02
Karolinska Sjukhuset, Stockholm S-17176, Sweden
FEATURES
SOURCE Location/Qualifiers
1. .1185
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
/tissue type="skin"
1. .1185
/gene="PSORS1C2"
325. .735
/gene="PSORS1C2"
/product="psoriasis susceptibility 1 candidate 2"
/protein_id="AA049377.1"
/db_xref="GI:28628835"
/translation="MTLNMKILGLVLCIHTRGISGSEGHSPHPADREAGSPITP
QGPVGDPPWPGAPPLFEDPPPTPSRPMRDLEPTGWPPEPPRTDPPQPRDDPWP
AGQPPENPWPAPAEVDNRPQEEPDIDPREYR"

CDS

ORIGIN

Alignment Scores:

Pred. No.:	2.55e-24	Length:	1185
Score:	808.00	Matches:	136
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-994-365-2 (1-136) x AF484420 (1-1185)

QY 1 MetIleuAsnTrpLysLeuLeuGlylleuValIleuCySteuHsThrArgGlylle 20
DB 325 ATGATCTCACTGAGAGCTCTGGGATCTGCTCTTGCTCGACACCAAGGATC 384
QY 21 SerGlySerGlyGlyHisProSerHisProProAlaGluAspArgGluGluAglYser 40
DB 385 TCAGGCGAGGAGGCGACCCCTCTCACCCCGCAGAGGACCGAGAGGAGGCGCTCC 444
QY 41 ProThreuProGlnGlyProProValProGlyAspProTrpProGlyAlaProProLeu 60
DB 445 CCAACATTTGCTCAGAGGCCCCCGGATCCCGGTGACCTTGCGCAGAGGAGGCGCTCTC 504
QY 61 PheGluAspProProTrpThrArgProSerArgProTrpArgAspLeuProGluThrGly 80
DB 505 TTGGAAGATCTCTCGCTTACCCGCCCAAGTCGTCTCTGAGAGACTGCTGAAACTGGA 564
QY 81 ValTrpProProGlnProProValProGlyAspProProGlnProProArgProAspAspPro 100
DB 565 GTCTGGCCCCCTGAAACCGCTAGAACGATCTCTCACTCTCCCGGCTGACGACCT 624
QY 101 TrpProAlaGlyProGlnProProGluAsnProTrpProProAlaProGluValAspAsn 120
DB 625 TGGCCGCGAGAGACCCGAGCCCGGAAACCCCTGCGCTCTGCGCTGAGGTGACAC 684
QY 121 ArgProGlnGluGluProAspLeuAspProProArgGluGluYrArg 136
DB 685 CGACCTCAGAGAGGAGCCACTAGACCCACCCCGGAAAGTACAGA 732

RESULT 5
AX406002 1473 bp DNA linear PAT 14-JUN-2002
LOCUS Sequence 417 from Patent WO0222660.
DEFINITION
AX406002.1 GI:21439443
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Tang,Y.T., Liu,C., Zhou,P., Asundi,V., Zhang,J., Zhao,Q.A., Ren,F.,
Xue,A.J., Yang,Y., Wehrman,T. and Drmanac,R.T.
TITLE Novel nucleic acids and polypeptides
JOURNAL Patent: WO 0222660-A 417 21-MAR-2002;
HYSEO, INC. (US)
FEATURES
SOURCE Location/Qualifiers

source 1..1473
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
636..1046
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD35109.1"
/db_xref="GI:21439444"
/translation="MTLNKRLGLIVLCITRGLSGSEGHSPHAPADREAGSPILP
QGPVREDPPWPGAPLFEEDPPPTPRSPRMDLDETGVWPEPPPTDPPQPRDDPMP
AGQPENPMPAPAEVNDNRPOEEDLDPPREXR"

ORIGIN

Alignment Scores:

Pred. No.:	2.98e-24	Length:	1473
Score:	808.00	Matches:	136
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-994-365-2 (1-136) x AX406002 (1-1473)

QY 1 MetIleuAsnTrpIleuGlyIleValIleuCysIleuHisTrnArgGlyIle 20
Db 636 ATGATCTCAACTGGAAGCTCTGGGATCTGTCTCTTGGCTGCACACAGAGGATC 695

QY 21 SerGlySerGluGlyHisProSerHisProProAlaGluAspArgGluGluAlaGlySer 40
Db 696 TCAAGGCGAGGCGGCGCCCTCTCACCCACCCGACAGAGACCGAGAGGCGAGGCTCC 755

QY 41 ProThrIeuProGlnGlyProProValProGlyAspProTrpProGlyValaProProIeu 60
Db 756 CCAACATTCGCTCAGGGCCCCCGCCAGTCCCGGTACCTTGGCCAGGAGGACCCCTCTC 815

QY 61 PheGluAspProProTrnArgProSerArgProTrpArgAspIeuProGluTrnGly 80
Db 816 TTGGAAGATCTCGCGCTACCGGCCAGTCGTCTCGAGAGACCTGCTGAACCTGGA 875

QY 81 ValTrpProProGluProProArgTrnAspProProGlnProProAlaGProAspPro 100
Db 876 GTCGGCCCCCTGAAACCGCTCAGAACGATCTCTCAACCTCCCGGCTGACGACCT 935

QY 101 TrpProAlaGlyProGlnProProGluAsnProTrpProProAlaProGluValaAspAsn 120
Db 936 TGGCCGACAGAACCCCGCCCGCCAGAAACCCCTGCTGCTCTGAGTGAGACAC 995

QY 121 ArgProGlnGluProAspIeuAspProProArgGluGluTrnArg 136
Db 996 CGACCTCAGAGGAGCGACGACCTAGACCCCGGAGAGATACAGA 1043

RESULT 6
AX477396 2997 bp DNA linear PAT 12-AUG-2002
LOCUS Sequence 10 from Patent WO0244375.
DEFINITION AX477396
ACCESSION AX477396
VERSION AX477396.1 GI:22216625
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
Charnley, P., Moss, P. and Mceuen, M.
TITLE Compositions and methods for diagnosing or treating psoriasis
JOURNAL Patent: WO 0244375-A 10 06-JUN-2002;
Celltech R & D, Inc. (US)

FEATURES
source Location/Qualifiers
1..2997
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.:	3.07e-20	Length:	2997
Score:	712.00	Matches:	118
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	88.12%	Indels:	0
DB:	6	Gaps:	0

US-09-994-365-2 (1-136) x AX477396 (1-2997)

QY 19 GlyIleSerGlySerGluGlyHisProSerHisProProAlaGluAspArgGluGluAla 38
Db 2201 GGATCTCAGAGGAGGCGGCGCCCTCTCACCCACCGACAGAGAGAGGCA 2260

QY 39 GlySerProThrIeuProGlnGlyProProValProGlyAspProTrpProGlyValaPro 58
Db 2261 GGCTCCCAACATTCGCTCAGGGCCCCCGCCAGTCCCGGTACCTTGGCCAGGGGCAACC 2320

QY 59 ProIeuPheGluAspProProTrnArgProSerArgProTrpArgAspIeuProGlu 78
Db 2321 CTTCTTTGAAGATCTCTCGCTACCGGCCAGTCGTCTCGAGAGACCTGCTGAA 2380

QY 79 ThrGlyValTrpProProGluProProArgTrnAspProProGlnProProArgProAsp 98
Db 2381 ACTGAGTCTGGCCCCCTGAAACCGCTCAGAACGATCTCTCAACCTCCCGGCTGAC 2440

QY 99 AspProTrpProAlaGlyProGlnProProGluAsnProTrpProProAlaProGluVal 118
Db 2441 GACCCCTGGCGGACAGAACCCCGCCCGCCAGAAACCCCTGGCTCTGAGGTG 2500

QY 119 AspAsnArgProGlnGluProProAspIeuAspProProArgGluGluTrnArg 136
Db 2501 GACACCGACCTCAGAGAGAGCGACCTAGACCCCGGAGAGATACAGA 2554

RESULT 7
AX477390 3001 bp DNA linear PAT 12-AUG-2002
LOCUS Sequence 4 from Patent WO0244375.
DEFINITION AX477390
ACCESSION AX477390
VERSION AX477390.1 GI:22216619
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
Charnley, P., Moss, P. and Mceuen, M.
TITLE Compositions and methods for diagnosing or treating psoriasis
JOURNAL Patent: WO 0244375-A 4 06-JUN-2002;
Celltech R & D, Inc. (US)

FEATURES
source Location/Qualifiers
1..3001
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.:	3.08e-20	Length:	3001
Score:	712.00	Matches:	118
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	88.12%	Indels:	0
DB:	6	Gaps:	0

US-09-994-365-2 (1-136) x AX477390 (1-3001)

QY 19 GlyIleSerGlySerGluGlyHisProSerHisProProAlaGluAspArgGluGluAla 38
Db 2205 GGATCTCAGAGGAGGCGGCGCCCTCTCACCCACCGACAGAGAGAGGCA 2264

Qy 39 GlysSerProThreupProgingluProProValProgluYAspProTrpProgluYAlaPro 58
|
Db 2265 GGCTCCCAACATTGGCTCTGAGGGGCCCCGAGTCCCGGTGACCTTGCGCCAGGGGCAACC 2324
Qy 59 ProleuphEgluAspProProProThArgProSerArgProTrpArgAspLeuProglu 78
|
Db 2325 CCTCTCTTAAAGATCTCCGCGCCCTACCCGCCGATGCTCCCTGAGAGACTCCCTGAA 2384
Qy 79 ThGlyValTrpProProgluProProArgThAspProProgluProProArgProAsp 98
|
Db 2385 ACTGAGATCTGGCCCCCTGAAACCGCTAGAACGATCTCTCAACCTCCCGGCTGAC 2444
Qy 99 AspProTrpProAlaGlyProgluInProProgluAsnProTrpProProAlaProgluVal 118
|
Db 2445 GACCCCTTGGCGGAGAGACCCGACCCCGAGAAACCCCTGCTGCTGCTGCGCTGAGGTG 2504
Qy 119 AspAsnArgProgluIngluProAspLeuAspProProArggluYArg 136
|
Db 2505 GACAAACGACCTCAGAGAGACCACTAGACCCACCCGCGAAGAGTACAGA 2558
RESULT 8
BD095297 25235 bp DNA linear PAT 27-AUG-2002
LOCUS The method of testing for psoriasis vulgaris.
DEFINITION BD095297
ACCESSION BD095297.1 GI:22640885
VERSION WO 0142458-A/2.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Inoko,H. and Taniya,G.
TITLE The method of testing for psoriasis vulgaris
JOURNAL Patent: WO 0142458-A 2 14-JUN-2001;
HIDETOSHI INOKO,GEN TANIYA
COMMENT OS Homo sapiens (human)
PN WO 0142458-A/2
PD 14-JUN-2001
PF 06-DEC-2000 WO 2000JP008624
PR 06-DEC-1999 JP 99P 346867
PI HIDETOSHI INOKO,GEN TANIYA
PC C12N15/12, C1201/68
CC The method of testing for psoriasis vulgaris
FH Key Location/Qualifiers
FT exon (1)..(1420)
FT exon (1282)..(1405)
FT exon (1602)..(1702)
FT exon (1602)..(1631)
FT exon (2352)..(2364)
FT exon (6287)..(6509)
FT exon (10417)..(10493)
FT exon (14244)..(14407)
FT exon (14244)..(14344)
FT exon (25190)..(25235).
FEATURES
source location/Qualifiers
1..25235
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 1,4e-19 Length: 25235
Score: 712.00 Matches: 118
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.12% Indels: 0
Gaps: 0
US-09-994-365-2 (1-136) x BD095297 (1-25235)
Qy 19 GlyIleSerGlySerGluGlyHisProSerHisProProAlaGluAspArgGluAla 38

Db 1754 GGATCTCAGGCGAGGCGCCACCCCTTCACCCAGCCAGAGAGCCAGAGGAGCA 1813
Qy 39 GlysSerProThreupProgingluProProValProgluYAspProTrpProgluYAlaPro 58
|
Db 1814 GGCTCCCAACATTGGCTCTGAGGGGCCCCGAGTCCCGGTGACCTTGCGCCAGGGGCAACC 1873
Qy 59 ProleuphEgluAspProProProThArgProSerArgProTrpArgAspLeuProglu 78
|
Db 1874 CCTCTCTTAAAGATCTCCGCGCCCTACCCGCCGAGTGTCTCTGAGAGACTGCTGAA 1933
Qy 79 ThGlyValTrpProProgluProProArgThAspProProgluProProArgProAsp 98
|
Db 1934 ACTGAGATCTGGCCCCCTGAAACCGCTAGAACGATCTCTCAACCTCCCGGCTGAC 1993
Qy 99 AspProTrpProAlaGlyProgluInProProgluAsnProTrpProProAlaProgluVal 118
|
Db 1994 GACCCCTTGGCGGAGAGACCCGACCCCGAGAAACCCCTGCTGCTGCTGCGCTGAGGTG 2053
Qy 119 AspAsnArgProgluIngluProAspLeuAspProProArggluYArg 136
|
Db 2054 GACAAACGACCTCAGAGAGACCACTAGACCCACCCGCGAAGAGTACAGA 2107
RESULT 9
AB088114/c 30911 bp DNA linear PRI 08-JAN-2003
LOCUS AB088114
DEFINITION Homo sapiens STG, S, SPR1, SEEK1 genes.
ACCESSION AB088114
VERSION AB088114.1 GI:27544424
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Shilina,T., Ota,M., Katsuyama,Y., Hashimoto,N. and Inoko,H.
TITLE Genome diversity in HLA: A new strategy for detection of genetic
polymorphisms in expressed genes within the HLA class III and class
I regions
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 30911)
AUTHORS Shilina,T.
TITLE Direct Submission
JOURNAL Submitted (08-JUL-2002) Takashi Shilina, Tokai University School of
Medicine, Molecular Life Science 2; Bohseida, Isehara, Kanagawa
259-1193, Japan (E-mail: tshilina@is.icc.u-tokai.ac.jp.
Tel:81-463-93-1121, Fax:81-463-94-8884)
FEATURES
source location/Qualifiers
1..30911
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.31"
/cell_line="LKT3"
/cell_type="B cell"
1317..2383
/number=2
/complement(join(1473..2383,2581..2647))
/gene="STG"
complement(join(1473..2383,2581..2647))
/gene="STG"
/codon_start=1
/product="hypothetical protein"
/protein_id="BAC54947.1"
/db_xref="GI:27544425"
/translation="MQGRVAGSCAPGLILVCLHLPGLFARSIGVBEKVSQNLGTNL
POLGPGSTGNSBHPQALDPRNDIARVPLKLSVYASGDFPPAGSAVORPSPW
GLPAMDSWPEDPWQWMAAARLALGEALPEELSYSAALAPGSGPLGESSPDAV
GLSPKSLHLDSESRRLPRNSLCAAGKTLSPRPSLIHRLPLPHPKNTLPNSVM
GGGGPTGWTGRMPHPPEGLIWGINQPGTGSWNINIKPGSGWGNINRYTGGSGWGNIN
RYPGSGWGNIHLYPGINPPPGVLRPPGSSWNI PAGFPNPPSRLQWG"
2581..2647
exon

exon
4938..4983
/number=1
/number=1
5185..7618
/number=2
gene
complement {join(6114..7618,10423..10459)}
/gene="S"
complement {join(6114..7618,10423..10459)}
/gene="S"
codon_start=1
/product="modified desmosin expressed in non-cornified epidermis"
/protein_id="BAC54948.1"
/db_xref="GI:27544426"
/translation="MMALLAGLLPGLTAKISGFSPDKDPFRITSPNDKCLTGKGGDSGSSFYSGSSSSGSSSISBARSSGGGSGSSSSS1AQGSSASAPRRTGYSGVSYSGSSYLQAGSGSQLOGSSSHSGSSGSHSGSSSSSFQFSSSFVGVNGSALPTNNYSYKGLINPSQPGSSSSSQTSGVSSGQVSSNQPCSSDIPSPCSGPIYVSHSGYIPSSHSVSGQRPVVVVVDQHGSGAGPVGQPCPSNGILPGKPEPTITVDKSYGGEVVGSSDSYLVPCMTYVSKGKIYVGFTKENVPKVSGVPSFAAGPISEGGKXYSNSNPITPSGSAASSAIAFOPVGTGVOQLCGGSGTSGKGPSPSSSVPSGSS1SSSSGSPVPCGSAQSPCSPGCTSPSSSSSGSGSKITLIQPCSKSSSSGHPMSYSITLTGPPGSPHPDPASGAKPCPSSSAGKIPCSITNDILAQVPLQPLADPEVFLPQSGLLDSP"
10423..10521
/number=1
15765..15928
/number=2
19676..19752
/number=3
27641..28413
/number=2
complement {join(28058..28413,29079..29133)}
/gene="SPR1"
complement {join(28058..28413,29079..29133)}
/gene="SPR1"
/codon_start=1
/product="hypothetical protein"
/protein_id="BAC54949.1"
/db_xref="GI:27544427"
/translation="MTINMKLTGITVLCIATHRGISGSRGSHSPADRRAGSPPLQGPPVPGDPMGAPLPEDPPPTPRSPKRWRLPRTGVWPPPPPTDTPQPPRPDDPMPFAGPPPPPPMPAPAEVNDPQEPPLDPEBREYR"
28537..28566
/number=4
28763..28886
/number=5
join(28864..28886,29748..30039)
/gene="SEEK1"
join(28864..28886,29748..30039)
/gene="SEEK1"
/codon_start=1
/product="hypothetical protein"
/protein_id="BAC54950.1"
/db_xref="GI:27544428"
/translation="MEPANHPWAGDIQAMISKEFHIAATQDDCKRGRTQEDILVPSSHPFLFASVLPWAPPEARLQOPPLPPPSGIHLSAARTLAFTLVYSSPSHSPGLASSLI"
29079..29448
/gene="SEEK1"
/number=1
29748..30167
/number=6

US-09-994-365-2(1-136) x AB088114 (1-30911)

OY 19 Gly11eserGlyerGluGlyVhiSProSerH1aProProAla1G1uAspArgGluGlu1a 38

Db 28414 GGCAATTCACAGACGAGGGCCACCCCTCTCACCCACCCGACAGAGACCGAAGAGAGCA 28355

OY 39 GlySerProThrLeuProGlnGlyProProValProGlyASPProTrpProGlyAlaPro 58

Db 28354 GGCTCCCAACATTGCTCTAGGGCCCCCAGTCCCGGTGACCTTGGCAAGGGCAACC 28295

OY 59 ProLeuPheGluAspProProProThrArgProSerArgProTrpArgAspLeuProGlu 78

Db 28394 CCTCTCTTTAAATGATCCTCCGCTTACCCCCACAGTCGTCCTGGAGAGACCTGCTGAA 28235

OY 79 ThrGlyValAlrProProGluProProAlaGlyThrAspProProGlu1ProProArgProAsp 98

Db 28234 ACTGAGATCTGGCCCCCTTGAACCGCTTGAAGCGAATCTCTTCAACTCTCCCGGCTGAC 28175

OY 99 AspProTrpProAlaGlyProGlnProProGluAsnProTrpProProAlaProGluAl 118

Db 28174 GACCTTTGGCGGACGAGACCCGACCCCGAAGAAACCTTGCGCTCTGCTCCCTGAGGTG 28115

OY 119 AspAsnArgProGlnGluGluProAspLeuAspProProArgGluGluTrpArg 136

Db 28114 GACAAACCACTCAGAGAGAGCAGCACTTGAAGCCACCCCGGAGAAAGTACAGA 28061

RESULT 10

AB023060

LOCUS AB023060 39196 bp DNA linear PRI 20-NOV-1999

DEFINITION Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region,

AB023060

ACCESSION AB023060

VERSION AB023060.1 GI:5672629

KEYWORDS HTG.

SOURCE

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (sites)

Shiina,T., Tamiya,G., Oka,A., Takishima,N., Yamagata,T.,

Kikawa,E., Iwata,K., Tomizawa,M., Okutaki,N., Kuwano,Y.,

Watanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,

Bahrami,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,

Bahram,S. and Inoko,H.

Molecular dynamics of MHC genesis unraveled by sequence analysis of

the 1,796,938-bp HLA class I region

Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)

JOURNAL

MEDLINE 20027539

PUBMED 10557312

REFERENCE 2 (bases 1 to 39196)

AUTHORS Shiina,T. and Takishima,N.

TITLE Direct Submission

JOURNAL Submitted (29-JAN-1999) Takashi Shiina, Tokai University School of

Medicine, Department of Molecular Life Science 2, Bohseidai,

Isehara, Kanagawa 259-1193, Japan

E-mail:tsshiina@ls.icc.u-tokai.ac.jp, Tel:81-463-93-1121,

Fax:81-463-94-8884)

location/Qualifiers

1..39196

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="6"

/map="6p21.3"

FEATURES

source

Alignment Scores:	
Pred. No.:	1.62e-19
Score:	712.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	88.12%
DB:	9
Gaps:	0
Length:	30911
Matches:	118
Conservative:	0
Mismatches:	0
Indels:	0

```
ORIGIN
Alignment Scores:
Pred. No.:      1.92e-19    Length:   39196
Score:          712.00     Matches:   118
Percent Similarity: 100.00% Conservative: 0
               /cell_line="BOLETH"
               /cristae_type="B cell line"
```

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 88.12% Indels: 0
 DB: 9 Gaps: 0
 US-09-994-365-2 (1-136) x AB023060 (1-39196)

QY 19 GYIYISeSerGlySerGlyGlyYHISProSerHisProProAlaGluAspArgGluGluAla 38
 DB 10634 GGCATCTCAAGCAGCGAGGGCCACCCCTCTACACCCAGCCAGAGAGAGAGCA 10693
 QY 39 GlySerProThrLeuProGlnGlyProProValProGlyAspProTyrProGlyAlaPro 58
 DB 10694 GGGTCCCAACATGCTCTCAGGGCCCCCAGTCCCGGTGACCTTGCCAGGGGCAACC 10753
 QY 59 ProLeuPheGluAspProProProProThrArgProSerArgProTyrPArgAspLeuProGlu 78
 DB 10754 CCTCTCTTAAAGTCTCTCCGCTACCCGCCAGTGTCTCTGAGAGACCTGCTGAA 10813
 QY 79 ThGlyValTyrProProGlnProProArgThrAspProProGlnProProArgProAsp 98
 DB 10814 ACTGGAGTCTGGCCCCCTGAAACCGCTAGAACGATCTCTCAACTCCCCGGCTGAC 10873
 QY 99 AspProTyrProAlaGlyProGlnProProGluAspProTyrProProAlaProGluVal 118
 DB 10874 GACCCCTTGCGCGGACAGACCCCAAGCCCAAGAAACCCCTGCGCTCTGAGGTG 10933
 QY 119 AspAspArgProGlnGluProAspLeuAspProProArgGluGluTyrArg 136
 DB 10934 GACACACGACCTCAGAGGAGCAGACCTAGACCCACCCGGGAGAGTACAGA 10987

RESULT 11

AC004195 40878 bp DNA linear PRI 08-DEC-1998
 LOCUS Homo sapiens clone UMGC:y24c027 from 6p21, complete sequence.
 AC004195
 AC004195.1 GI:3980474

DEFINITION Homo sapiens (human)
 VERSION AC004195.1
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 40878)
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Jener, M., Guillaudoux, T., Vu, Q., Kulyavin, T., Harter, H. and Geraghty, D. E.

TITLE Large scale sequence analysis of the human MHC class I region
 JOURNAL Unpublished (1998)
 REMARK Fred Hutchinson Cancer Research Center
 The Clinical Research Division
 1100 Fairview Ave. N., P.O. Box 19024
 Seattle, WA 98109-1024

REFERENCE 2 (bases 1 to 40878)
 AUTHORS Geraghty, D. E. and Olson, M. V.
 JOURNAL Direct Submission
 Submitted (23-FEB-1998) Human Genome Center, University of
 Washington, Box 352145, Seattle, WA 98195, USA

REFERENCE 3 (bases 1 to 40878)
 AUTHORS Geraghty, D. E. and Olson, M. V.
 JOURNAL Direct Submission
 Submitted (08-DEC-1998) Human Genome Center, University of
 Washington, Box 352145, Seattle, WA 98195, USA

REFERENCE 4 (bases 1 to 40878)
 AUTHORS Geraghty, D. E. and Olson, M. V.
 JOURNAL Direct Submission
 Submitted (08-DEC-1998) Human Genome Center, University of
 Washington, Box 352145, Seattle, WA 98195, USA

REFERENCE 5 (bases 1 to 40878)
 AUTHORS Geraghty, D. E. and Olson, M. V.
 JOURNAL Direct Submission
 Submitted (08-DEC-1998) Human Genome Center, University of
 Washington, Box 352145, Seattle, WA 98195, USA

COMMENT On Dec 8, 1998 this sequence version replaced gi:2905865.
 Overlapping Sequences:
 5': UMGC:y14c057 (Genbank Accession: AC006047)
 3': UMGC:y24c203

Quality levels above 40 are expected to have less than
 1 error in 10,000 bp.
 Base-by-base quality values are not generally visible from the
 Genbank flat file format but are available as part
 of this entry's ASN.1 file.

Double stranded (DS) coverage: 77.6%
 DS or two chemistry coverage: 100.0%
 Single stranded regions: 0

Sequence Validation:

This sequence has been validated by Multiple Complete Digest
 Mapping. Comparison of the experimentally derived map digest
 fragments with sequence-predicted fragments is given below.
 Small fragments below a variable cutoff (approximately 400-600bp)
 are not mapped and hence do not appear in the table. There are no
 significant remaining discrepancies between the experimental and
 predicted values. Uniquely ordered fragment groups are separated
 by dashed lines.

Map	BglII	Seq	HindIII	Seq	Map	NsiI	Seq
5056.53	5005.00	979.90	957.00	8811.76	8685.00		
2289.48	2257.00	3644.92	3580.00	9333.67	9154.00		
5302.18	5207.00	5611.48	5525.00	814.06	801.00		
894.03	880.00	4618.79	4525.00	10116.87	9863.00		
3041.57	2999.00	1532.79	1530.00	2432.75	2413.00		
14697.70	14691.00	1726.25	1724.00				
		1479.40	1473.00				
		909.61	880.00				
		8223.42	7996.00				
		2404.83	2380.00				
		7342.43	7194.00				

FEATURES

Source Location/Qualifiers
 1..40878
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="6p21"
 /clone="CGM1:A194D6"
 /sub_clone="UMGC:y24c027"
 /cell_line="CGM1"
 /clone_lib="Wash U YAC Library"
 complement(4237..4519)
 /rpt_family="Alu"
 repeat_region
 complement(4643..5052)
 /rpt_family="Alu"
 repeat_region
 5090..5149
 /rpt_family="MIR"
 repeat_region
 9346..9586
 /rpt_family="Alu"
 complement(9800..10094)
 /rpt_family="Alu"
 repeat_region
 11553..11834
 /rpt_family="Alu"
 repeat_region
 12152..12410
 /rpt_family="Alu"
 repeat_region
 12650..13079
 /rpt_family="Alu"
 complement(13117..13401)
 /rpt_family="Alu"

```
repeat_region      complement (15576..15686)
                    /rpt_family="Alu"
repeat_region      /rpt_family="Alu"
                    1571..15969
repeat_region      /rpt_family="Alu"
                    complement (16248..16536)
repeat_region      /rpt_family="Alu"
                    complement (17434..17719)
repeat_region      /rpt_family="Alu"
                    complement (17993..18283)
repeat_region      /rpt_family="Alu"
                    complement (19046..19327)
repeat_region      /rpt_family="Alu"
                    20915..21197
repeat_region      /rpt_family="Alu"
                    complement (21343..21613)
repeat_region      /rpt_family="Alu"
                    23590..23889
repeat_region      /rpt_family="Alu"
                    complement (23940..24065)
repeat_region      /rpt_family="Alu"
                    24066..24312
repeat_region      /rpt_family="Alu"
                    complement (24673..24731)
repeat_region      /rpt_family="Alu"
                    complement (24760..25051)
repeat_region      /rpt_family="Alu"
                    complement (27927..28526)
repeat_region      /rpt_family="Alu"
                    complement (28990..29269)
repeat_region      /rpt_family="Alu"
                    complement (29340..29635)
repeat_region      /rpt_family="Alu"
                    29889..30145
repeat_region      /rpt_family="Alu"
                    30290..30564
repeat_region      /rpt_family="Alu"
                    30791..31421
repeat_region      /rpt_family="Alu"
                    complement (32533..33421)
repeat_region      /rpt_family="Alu"
                    complement (33782..34080)
repeat_region      /rpt_family="Alu"
                    34426..35134
repeat_region      /rpt_family="Alu"
                    complement (35292..35444)
repeat_region      /rpt_family="Alu"
                    complement (37575..37780)
repeat_region      /rpt_family="Alu"
                    complement (40436..40717)
repeat_region      /rpt_family="Alu"

ORIGIN
Alignment Scores:
Pred. No.:          1.98e-19      Length:      40878
Score:              712.00        Matches:      118
Percent Similarity: 100.00%       Conservative: 0
Best Local Similarity: 100.00%    Mismatches:  0
Query Match:        88.12%        Indels:       0
DB:                  9            Gaps:         0

US-09-994-365-2 (1-136) x AC004195 (1-40878)
QY      19  G|Y|I|S|e|r|G|y|S|e|r|G|u|G|y|H|s|P|r|o|S|e|r|H|s|P|r|o|A|l|a|g|u|A|s|P|a|r|g|u|G|u|A|a| 38
Db      27088 GGGCTCTCAAGGCGAGGGGCGACCCCTCTCAACCCGAGAGGAGCCGAGAGGAGGCA 27147
QY      39  G|Y|S|e|r|P|r|o|H|e|u|P|r|o|G|u|G|y|P|r|o|V|a|P|r|o|G|y|A|s|P|r|o|T|P|r|o|G|y|A|l|a|P|r|o| 58
Db      27148 GGGCTCCCAACATTGGCTCTAGGGGCCCCCGAGTCCCGGTACCTTGCCAGGGGCAACC 27207
QY      59  P|r|o|L|e|u|P|r|o|P|r|o|P|r|o|P|r|o|P|r|o|P|r|o|P|r|o|P|r|o|P|r|o|P|r|o|P|r|o|P|r|o|P|r|o|P|r|o| 78
Db      27208 CCTCTTTGAAGATCTCTCGCGCTACCCGCGCGAGTGTCTCTGAGAGACCTGCTGAA 27267
```

```
QY      79  T|H|G|V|a|I|T|P|r|o|P|r|o|G|u|P|r|o|P|r|o|A|r|g|T|H|A|s|P|r|o|P|r|o|G|u|P|r|o|P|r|o|A|r|g|P|r|o|A|s|P| 98
Db      27268 ACTGAGAGTCTGGGCCCCCTGAGACCGCCTTAGAGAGATCTCTCACTCACTCCCGGCTGAC 27327
QY      99  A|s|P|r|o|T|P|r|o|A|l|a|G|y|P|r|o|G|u|P|r|o|P|r|o|G|u|A|s|P|r|o|T|P|r|o|P|r|o|A|l|a|P|r|o|G|u|A| 118
Db      27328 GACCTTGGCGCGCAGAGACCCCGCCCGAGAAACCTTGGCTCTGCTGCTGAGGTG 27387
QY      119 A|s|P|a|s|A|r|g|P|r|o|G|u|G|u|P|r|o|A|s|P|a|s|P|r|o|P|r|o|A|r|g|u|G|u|T|Y|Z|A|Y| 136
Db      27388 GACACCGAGCCTTAGAGAGGCCAGACTAGACCCACCCGGAGAGTACAGA 27441

RESULT 12
LOCUS      AX522117          55050 bp      DNA      linear      PAT 24-OCT-2002
DEFINITION Sequence 4 from Patent WO02064831.
ACCESSION  AX522117
VERSION     AX522117.1  GI:24411002
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1
AUTHORS     Lench,N.J., Allen,M.J. and Nicholls,R.K.
TITLE       Test and model for inflammatory disease
JOURNAL     Patent: WO 02064831-A 4 22-AUG-2002;
            Oxagen Limited (GB)
FEATURES
            Location/Qualifiers
            source          1..55050
                           /organism="Homo sapiens"
                           /mol_type="unassigned DNA"
                           /db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.:          2.45e-19      Length:      55050
Score:              712.00        Matches:      118
Percent Similarity: 100.00%       Conservative: 0
Best Local Similarity: 100.00%    Mismatches:  0
Query Match:        88.12%        Indels:       0
DB:                  6            Gaps:         0

US-09-994-365-2 (1-136) x AX522117 (1-55050)
QY      19  G|Y|I|S|e|r|G|y|S|e|r|G|u|G|y|H|s|P|r|o|S|e|r|H|s|P|r|o|A|l|a|g|u|A|s|P|a|r|g|u|G|u|A|a| 38
Db      27099 GGCATCTCAAGGCGAGGGGCGACCCCTCTCAACCCGAGAGGAGCCGAGAGGAGGCA 27158
QY      39  G|Y|S|e|r|P|r|o|H|e|u|P|r|o|G|u|G|y|P|r|o|V|a|P|r|o|G|y|A|s|P|r|o|T|P|r|o|G|y|A|l|a|P|r|o| 58
Db      27159 GGGCTCCCAACATTGGCTCTAGGGGCCCCCGAGTCCCGGTACCTTGCCAGGGGCAACC 27218
QY      59  P|r|o|L|e|u|P|r|o|P|r|o|P|r|o|P|r|o|P|r|o|P|r|o|P|r|o|P|r|o|P|r|o|P|r|o|P|r|o|P|r|o|P|r|o|P|r|o| 78
Db      27219 CCTCTTTGAAGATCTCTCGCGCTACCCGCGCGAGTGTCTCTGAGAGACCTGCTGAA 27278
QY      79  T|H|G|V|a|I|T|P|r|o|P|r|o|G|u|P|r|o|P|r|o|A|r|g|T|H|A|s|P|r|o|P|r|o|G|u|P|r|o|P|r|o|A|r|g|P|r|o|A|s|P| 98
Db      27279 ACTGAGAGTGGGCCCCCTGAGACCGCCTTAGAACGATCTCTCACTCCCGGCTGAC 27338
QY      99  A|s|P|r|o|T|P|r|o|A|l|a|G|y|P|r|o|G|u|P|r|o|P|r|o|G|u|A|s|P|r|o|T|P|r|o|P|r|o|A|l|a|P|r|o|G|u|A| 118
Db      27339 GACCTTGGCGCGCAGAGACCCCGCCCGAGAAACCTTGGCTCTGCTGCTGAGGTG 27398
QY      119 A|s|P|a|s|A|r|g|P|r|o|G|u|G|u|P|r|o|A|s|P|a|s|P|r|o|P|r|o|A|r|g|u|G|u|T|Y|Z|A|Y| 136
Db      27399 GACACCGAGCCTTAGAGAGGCCAGACTAGACCCACCCGGAGAGAGTACAGA 27452

RESULT 13
LOCUS      AL662867/c          70288 bp      DNA      linear      PRI 24-APR-2002
```

DEFINITION	Human DNA sequence from clone Xbac-34d1 on chromosome 6, complete sequence.
ACCESSION	AL662867
VERSION	AL662867.5
KEYWORDS	GI:20068664
SOURCE	HTG.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens (human)
AUTHORS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1
JOURNAL	Sycamore, N.
COMMENT	Direct Submission Submitted (23-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: clonerequest@sanger.ac.uk humquerry@sanger.ac.uk Clone request: clonerequest@sanger.ac.uk On Apr 7, 2002 this sequence version replaced gi:19309560. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Xbac-34d1 is from a CHORI-502 human bac - COX cell line library VECTOR: pYABAC2.1 This sequence was generated from part of bacterial clone contigs constructed by the MHC Haplotype Consortium and collaborators. Further information can be found at http://www.sanger.ac.uk/HGP/Chre/MHC. Location/Qualifiers 1..70288 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="6" /clone="Xbac-34d1" /clone_1fb="CHORI-502"
FEATURES	
SOURCE	
ORIGIN	
Alignment Scores:	
Pred. No.:	2.91e-19
Score:	712.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	88.12%
DB:	Gaps: 9
US-09-394-365-2 (1-136) x AL662867 (1-70288)	
QY	19 G1y1seerthlysergluglyhiaproseshiaprobiaagluasparglugluia1a 38
Db	67723 GGCAATCCAGACGAGCGGCGCCACCCCTTCACCCACCCGCAAGACGAGGAGGCA 67664
QY	39 G1y5erProthreupProginlyProProValjProglYAspProtrpProglYlaPro 58
Db	67663 GGCTCCCAACATTGCTCTCAGGGGCCCCCAAGTCCCGGTGATCCCTTGCCAGGGGCAACC 67604
QY	59 ProleubhegluapProProProthriarjProSeArjProtrPArjgaAspleuProglu 78
Db	67603 CCTCTCTTTGAAGATCTCTCGGCTACCCGCGCCAGTCGTCCCTGAGAGACCTCGCTGA 67544
QY	79 ThrclyValtrpProProgluProProArjgthThAspProProgluProProArjgProab 98

Df	67543	ACTGGAATCTGGCCCCCTGAACCGCCTTAAAGCAAGATCTCTCAACTCCCGGCCTGAC	6748
Oy	99	AspProTrpProAlaGlyProGlnProProGluAnbProITrpProProAlaProGluVal	118
Df	67483	GACCCTTGCCGGGAGGACCCCGACGCCCGAAGAACCCCTTGACCTCTCGCCCTGAAGGTG	6742
Oy	119	AspAsnArgProGlnGlnGluIleProAspLeuAspProTrpArgGluGlyTrpArg	136
Df	67423	GACAAACGACCTCAGAGAGACCAAGACTGACCAACCCCGGAAGAATAACA	67370
RESULT 14			
LOCUS	AP000510		
DEFINITION	Homo sapiens genomic DNA, chromosome 6p21.3, HLA Class I region,		
ACCESSION	AF000510 BA000025		
VERSION	AP000510.2 GI:7380878		
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
JOURNAL			
REFERENCE			
AUTHORS	Shima,S., Tamiya,G., Oka,A. and Inoko,H.		
TITLE	Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region		
JOURNAL	Published Only in Database (1999)		
REFERENCE	2 (bases 1 to 99999)		
AUTHORS	Hirakawa,M., Yamaguchi,H., Imai,K. and Shimada,J.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-SEP-1999) Mika Hirakawa, Japan Science and Technology Corporation (JST), Advanced Databases Department, 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081, Japan [E-mail:mike@tokyo.jst.go.jp, URL:http://www-alis.tokyo.jst.go.jp/, Tel:81-3-5214-8491, Fax:81-3-5214-8470]		
COMMENT	On Mar 31, 2000 this sequence version replaced gi:5926697. This sequence is conducted by Tokai University as a JST sequencing team. Principal Investigator: Hidetoshi Inoko Ph.D Phone:+81-463-93-1121, Fax:+81-463-94-8884, The sequence is submitted by Human Genome Sequencing in ALIS project of JST Japan Science and Technology Corporation (JST) 5-3, Yonbancho, Chiyoda-ku, Tokyo, 102-0081 Japan For further information about this sequences, please visit our sequence archive web site (http://www-alis.tokyo.jst.go.jp/HGS/top.html) or send email to webmaster@www-alis.tokyo.jst.go.jp Sequence updated (28-Mar-2000). Location/Qualifiers 1. .99999 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="6" /map="6p21.3" 2016..2435 /gene="SBEK1" 2016..2435 /gene="SBEK1" /number=6 complement(join(2144..2435,3297..3319)) /gene="SBEK1" complement(join(2144..2435,3297..3319)) /gene="SBEK1" /codon_start=1 /protein_id="BAB63314.1" /db_xref="GI:15277221" /tranlation="MEPAHFVMAADGLQAMISKKEFLIAATODCDCKRGRTQEDILVSS HPPLFASVLPMAPEEAARLQQPQLPPPSGSIHSASRTIALPTLVSSPSHSFGLSS LI" join(2735..3104,3770..4542) /gene="SRP1" 2735..3104		
FEATURES			
SOURCE			
gene			
CDS			
exon			
gene			
exon			

```

/gene="SPR1"
/number=1
join(3050..3104,3770..4125)
/gene="SPR1"
/codon_start=1
/protein_id="BAB63315.1"
/db_xref="GI:15277222"
/translation="MTLNMKLLGLVLCILHTRGISGSEGHSPHPADREHAGSPILP
AGQPPBNMPPAPEDVNRQSEPDLPPEEYR"
/gene="SEEK1"
join(3297..3420,3617..3646)
/number=5
/gene="SEEK1"
3617..3646
/gene="SEEK1"
/number=4
3770..4542
/gene="SPR1"
/number=2
12432..16422
/gene="SEEK1"
12432..12508
/gene="SEEK1"
/number=3
16259..16422
/gene="SEEK1"
/number=2
21667..27003
/gene="US"
21667..21765
/gene="US"
/number=1
join(21729..21765,24570..26074)
/gene="US"
/codon_start=1
/protein_id="BAB63316.1"
/db_xref="GI:15277223"
/translation="MMALLAGLLPGLTAKSITGTPSPCKDPRTITSPNDPLTGK
DSGFSYSGSSSSSGSISARSGGSSSGSSSIAQSGKAGFRPGTGYQVRS
SGSSSLQAGSGSQLGSSSHSGSSSGSSSHSSSFQFSSSFQVNGSL
PTNDNYRGLINPSQPCQSSSSQTSQSSSGQSVSNRQPCSDIPDSPCGPIVS
HSPYIPSSHSVSGQRPVVVVDHSGGAPVQGPCCNGILPGPCPITSVKX
YGVGVVGGSSDYLVPMTYSGKTIYGVYPTKENVKGSPPGVSPAAAPISSEKY
FSSNPRIPOSASASAIARQPVCTGVLGGSTGKSPSSSPVSSSSISSS
GSYHPCGSASQSPCPPTGTGTSRSSSSSSSGKITIIPCCGSSSSSGHPCMSVSLT
LTGCPDGSPPHPSAKKPCGSSSAGKIPCRSIRDLIAQVPLQIADPEVLPQGE
LIDSP"
exon      24570..27003
           /gene="US"
           /number=2
           26711..26940
           /gene="US"
           /note="RH17634;The location is between each flanking site
           of PCR primers."
           /db_xref="GDB:4572035"
           27205..27250
           /gene="SEEK1"
           27205..27250
           /gene="SEEK1"
           /number=1
gene
exon

```

ORIGIN

Alignment Scores:

```

Pred. No.:      3.74e-19      Length:      99999
Score:          712.00       Matches:      118
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:     88.12%      Indels:      0
DB:              9          Gaps:      0

```

US-09-994-365-2 (1-136) x AF000510 (1-99999)

```

QY      19  GYLLSErGlySerGIuGlyHISProSerHISProProAlaGIuAspArgGIuGIuAla 38
Db      3769 GCGATCTCAGGACGACGAGGCCACCCCTCTACCCACCCGAGAGGACGAGAGGCA 3828
QY      39  GYSerProThrIeuProGIuGlyProProValProGIuAspProTrProGIuAlaPro 58
Db      3829 GGCTCCCAACATGTCCTCAGAGGCCCCCAAGTCGCCGAGACCTTCGGCCAGGGGACACC 3888
QY      59  ProIeuPhuGIuAspProProProThrArgProSerArgProTrIpaArgAspIeuProGIu 78
Db      3889 CCTCTCTTGAAATCTCTCGCTACCCGCCAGTCGTCTCTGGAGAGCTGCTGAA 3948
QY      79  ThrGIuValTrProProGIuProProArgTrIpaArgProProGIuProProArgProAsp 98
Db      3949 ACTGAGAGTCTGGCCCCCTGACCCGCTAGAGGAGATCTCTCACTCCCGGCTGAC 4008
QY      99  AspProTrProAlaGIuGIuProGIuProProGIuAspProTrProProAlaProGIuAla 118
Db      4009 GACCCCTGGCCGACAGACCCCAAGCCCAAGAAACCTGCGCTCTGCTGAGGTG 4068
QY      119 AspAsnArgProGIuGIuGIuProAspIeuAspProProArgGIuGIuTrArg 136
Db      4069 GACACCCGACCTCAGAGAGCCAGACCTAGACCCACCCGGAAGAGTACAGA 4122

RESULT 15
AL773544/c
LOCUS      AL773544
DEFINITION Human DNA sequence from clone DAQB-18511 on chromosome 6, complete
sequence.
ACCESSION AL773544
VERSION   AL773544.5  GI:37805611
KEYWORDS  HTG.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE
  AUTHORS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  TITLE    Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
  JOURNAL  1 (bases 1 to 113388)
  COMMENT  Submitted (21-OCT-2003) Wellcome Trust Sanger Institute, Hinxton,
  Direct Submissions
  Cambridge, CB10 1SA, UK. E-mail enquiries:
  humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
  On Oct 21, 2003 this sequence version replaced gi:22759515.
  ----- Genome Center
  Center: Wellcome Trust Sanger Institute
  Center code: SC
  Web site: http://www.sanger.ac.uk
  Contact: humquery@sanger.ac.uk
  -----
  During sequence assembly data is compared from overlapping clones.
  Where differences are found these are annotated as variations
  together with a note of the overlapping clone name. Note that the
  variation annotation may not be found in the sequence submission
  corresponding to the overlapping clone, as we submit sequences with
  only a small overlap as described above.
  The following abbreviations are used to associate primary accession
  numbers given in the feature table with their source databases:
  Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information
  on the WORMPEP database can be found at
  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
  was generated from part of bacterial clone contigs constructed by
  the MHC Haplotype Consortium and collaborators. Further information
  can be found at
  http://www.sanger.ac.uk/HGP/Chr6/MHC
  This sequence was finished as follows unless otherwise noted: all
  regions were either double-stranded or sequenced with an alternate
  chemistry or covered by high quality data (i.e., phred quality >=
  30); an attempt was made to resolve all sequencing problems, such
  as compressions and repeats; all regions were covered by at least
  one plasmid subclone or more than one M13 subclone; and the
  assembly was confirmed by restriction digest, except on the rare
  occasion of the clone being a YAC.

```

DAOB-18511 is from a DNA-arts QBL human bac library VECTOR:

pBelOBAC11.

FEATURES

location/Qualifiers
1. 113388
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/clone="DAOB-18511"
/clone_1id="DNA-arts-BAC.1-QBL.1"

ORIGIN

Alignment Scores:

Pred. No.:	4.1e-19	Length:	113388
Score:	712.00	Matches:	118
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	88.12%	Indels:	0
DB:	9	Gaps:	0

US-09-994-365-2 (1-136) x AL773544 (1-113388)

```
QY      19  G|Y|I|e|e|g|y|s|e|r|g|u|g|y|h|i|s|p|r|o|s|e|r|h|i|s|p|r|o|a|l|a|g|l|u|a|s|p|a|r|g|l|u|a|l|a 38
         |||
Db      60143  GGCATCTCAGGCGAGCGGCGCACCTCTCACACCGCAGAGACCGAGAGAGGCA 60084

QY      39  G|Y|s|e|r|p|r|o|t|h|r|e|u|p|r|o|g|i|n|g|l|p|r|o|p|r|o|v|a|l|p|r|o|g|l|y|a|s|p|p|r|o|t|p|r|o|g|l|y|a|l|a|p|t|o 58
         |||
Db      60083  GGCTCCCAACATTGGCTTCAGGGGCCCTCCAGTCCCGGTGACCTTGCCGCGAGGGCACCC 60024

QY      59  P|r|o|l|e|u|p|h|e|g|l|u|a|s|p|r|o|p|r|o|t|h|r|a|r|g|p|r|o|s|e|r|a|r|g|p|r|o|t|r|p|a|r|g|a|s|p|l|e|u|p|r|o|g|l|u 78
         |||
Db      60023  CCTCTCTTTGAAAGATCTCCGCCCTACCGGCCCAAGTCGTCCCTGGAGAGACTGCTGAA 59964

QY      79  T|h|r|g|l|y|a|l|t|r|p|r|o|p|r|o|g|l|u|p|r|o|p|r|o|a|r|g|t|h|r|a|s|p|r|o|p|r|o|g|i|n|p|r|o|p|r|o|a|r|g|p|r|o|a|s|p 98
         |||
Db      59963  ACTGGAGTCTGGCCCCCTGAAACCGCTAGAACGGATCTCTCAACCTCCCGGCTTGAC 59904

QY      99  A|s|p|p|r|o|t|r|p|r|o|a|l|a|g|l|p|r|o|g|i|n|p|r|o|p|r|o|g|l|u|a|s|p|r|o|t|r|p|r|o|p|r|o|a|l|a|p|r|o|g|l|u|a|l 118
         |||
Db      59903  GACCCCTTGGCCGGAGAGACCCCAACCCCAAGAAACCCCTGGGCTCTGCCCCCTGAGGTTG 59844

QY      119  A|s|p|a|s|n|a|r|g|p|r|o|g|i|n|g|i|u|p|r|o|a|s|p|l|e|u|a|s|p|r|o|p|r|o|a|r|g|l|u|g|i|u|y|r|a|r|g 136
         |||
Db      59843  GACCAACGACCTCAGAGAGACCGACGACTGACCCCGGAGAGAGTACAGA 59790
```

Search completed: January 11, 2005, 13:58:18
Job time : 3765.76 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OW protein - nucleic search, using frame_plus.p2n model

Run on: January 11, 2005, 11:40:34 ; Search time 2821.18 Seconds
(without alignments)
1756.640 Million cell updates/sec

Title: US-09-994-365-2
Perfect score: 808
Sequence: 1 MIMMMLGLIVLCLHTRGI.....EVDNRPEBDDLPREYR 136

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 segs, 18219865908 residues
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DRV=xlh
-Q=/cgn2_1/USPTO.epool_h/US0994365/runat.10012005.172232.6834/app.query.fasta_1.590
-DB=EST -OPMT=faa1ap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=bloum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pcr -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0994365 @CGC 1.1.4385 @runat.10012005.172232.6834 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBIOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WANT TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gsa1.*
9: gb_gsa2.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	646	80.0	634	7	CF764947	CES003088
2	619	76.6	593	7	CF765720	CES001471
3	617	76.4	383	2	AM315342	12593 MAR
4	536.5	66.4	422	1	AI596929	v146e11.y
5	528.5	65.4	562	1	AA530301	AA530301
6	510.5	63.2	451	9	CG484009	OST17807
7	507	62.7	416	9	CG481452	OST13885
8	506	62.6	669	9	CG484609	OST18617
9	501	62.0	442	9	CG487403	OST22893

10	471.5	58.4	475	9	CG473878	CG473878 OST1668 M
11	460	56.9	322	9	CG474695	CG474695 OST2738 M
12	446.5	55.3	332	1	AA763309	AA763309 vW99h03.r
13	441	54.6	366	9	CG474680	CG474680 OST2720 M
14	425	52.6	451	1	AA798896	AA798896 vW94e08.r
15	375	46.4	395	9	CG528207	CG528207 OST107284
16	363	44.9	283	9	CG474588	CG474588 OST2599 M
17	345	42.7	243	8	AQ357151	AQ357151 CTRBI-B1-
18	298	36.9	204	1	AA733661	AA733661 vW74f01.r
19	283	35.0	379	1	AA791103	AA791103 vW14d02.r
20	233	28.8	489	8	BH098389	BH098389 RPCT-24-3
21	221	25.9	984	4	BG441224	BG441224 GA_Ea001
22	209	25.9	1380	9	CL058490	CL058490 CH216-88C
23	206	25.5	361	1	AA168568	AA168568 m31c08.r
24	205.5	25.4	812	9	AG133085	AG133085 Pan trogl
25	205.5	25.4	1218	9	AG435362	AG435362 Mus muscu
26	205	25.4	1272	9	AG365674	AG365674 Mus muscu
27	205	25.4	1283	9	AG435406	AG435406 Mus muscu
28	204.5	25.3	1585	8	CC294035	CC294035 CH261-82A
29	204.5	25.3	1691	9	AG341104	AG341104 Mus muscu
30	203.5	25.2	898	5	B0411951	B0411951 GA_Ea004
31	203.5	25.2	977	9	CL488066	CL488066 SATL_503
32	203	25.1	848	9	CNS021YE	AL220271 Tetracodon
33	202.5	25.1	837	4	BG530104	BG530104 602558771
34	202	25.0	1142	9	CL501710	CL501710 SATL_702
35	202	25.0	1509	9	CL476587	CL476587 SATL_258
36	201.5	24.9	688	8	A2197670	A2197670 SP_1035_B
37	201.5	24.9	686	8	BZ041090	BZ041090 11112601
38	201	24.9	1051	9	CL119109	CL119109 ISB1-75W6
39	201	24.9	2131	8	CC296269	CC296269 CH261-104
40	200.5	24.8	628	6	CD890919	CD890919 G118.115L
41	200.5	24.8	738	5	B0805842	B0805842 WHE3571.F
42	200.5	24.8	738	5	CK196627	CK196627 FGAS00508
43	200.5	24.8	1094	7	CC908599	CC908599 t043p13ba
44	200.5	24.8	1100	8	CC262597	CC262597 t043p13ba
45	200.5	24.8	1337	9	CL478195	CL478195 SATL_285

ALIGNMENTS

RESULT 1
CF764947
LOCUS
DEFINITION CES003088 Bos taurus skin cDNA library Bos taurus cDNA clone
ACCESSION CF764947
VERSION CF764947.1 GI:37714166
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE
AUTHORS Wang, Y.H., McWilliam, S. and Iehner, S.
TITLE Transcription profiling of cattle skin
JOURNAL Unpublished (2003)
COMMENT Contact: Dr Yonghong Wang
Functional Genomics Lab
CSIRO Livestock Industries
Level 5, Queensland Biosciences Precinct, University of Queensland,
306 Carmody Road St. Lucia QLD Australia
Tel: 07 3214 2445
Fax: 07 3214 2685
Email: Yonghong.Wang@csiro.au
Plate: 40 row: G column: 07.
Location/Qualifiers
1. .634
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Hereford Shorthorn"
/db_xref="taxon:9913"
/clone="CCL003088"

FEATURES
source

```

/sex="female"
/tissue_type="pooled"
/dev_stage="Adult"
/lab_host="XJ1-BlueMRP strain"
/clone_id="Bos taurus skin cDNA library"
/notes="Organ: skin; Vector: Uni-ZAPXR; Site 1: EcorI;
Site 2: Xho I; Library made from pooled skin of adult
female Hereford-Shorthorn."

```

ORIGIN

Alignment Scores:

```

Pred. No.: 9,56e-31 Length: 634
Score: 646.00 Matches: 109
Percent Similarity: 85.19% Conservative: 6
Best Local Similarity: 80.74% Mismatches: 20
Query Match: 79.95% Indels: 0
DB: Gaps: 0

```

US-09-994-365-2 (1-136) x CF764947 (1-634)

```

QY 2 TleuAsnTTrpLysLeuGlyTleuValLeuCySteuHisThrArgIYIleSer 21
Db 13 ATGCTCAACTGGAACCTCTAGGATCTGTCTTGTCTTGTCTGAGGATCTCA 72
QY 22 GlysSerGIuGlyHisProSerHisProProAlaGluAspArgGluGluAlaGlySerPro 41
Db 73 GGCACTGGAACCAAGCTTCCCTCTCATCCAGAGAGATCTCAGAGAGAGAGGCGCTCCA 132
QY 42 ThrLeuProGlnGlyProProValProGlyAspProTrpProGlyAlaProProLeuPhe 61
Db 133 CCAATGGCTCAGGGGCCCCCAATCCTGTGTGACCCCTGGCCAGGGGCAACCCCGCTCTT 192
QY 62 GluAspProProProTrpArgProSerArgProTrpArgAspLeuProGluThrGlyVal 81
Db 193 GAGGATCTCTCACTCCAGGCCCCCAATCGTCTCGAGAGACCTGCTGATTCGAGTC 252
QY 82 TrpProProGluProProArgThrAspProProGlnProProAlaProArgProAspAspProTrp 101
Db 253 TGGCTCTTAACCCCTTAAGATGATCCCTCAACTCTCGGCTGAGACACCCCTTG 312
QY 102 ProAlaGlyProGlnProProGluAsnProTrpProProAlaProGluValAspAsnArg 121
Db 313 CCGCAGAGACCCCGAGCTCCAGAAACCCCTGGCCACCTGAGGTGAGACACGGA 372
QY 122 ProGlnGluGluProAspLeuAspProProArgGluGluGlyTrpArg 136
Db 373 TCTCAGAGAGCCAGACCTTGACCCACCCAGGAGAGATACAGA 417

```

```

RESULT 2
CF765720 593 bp mRNA linear EST 17-OCT-2003
LOCUS CDS001471 Bos taurus skin cDNA library Bos taurus cDNA clone
ACCESSION CCF765720
VERSION CCF765720.1 GI:37714939
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

```

```

REFERENCE
AUTHORS Wang,Y.H., McWilliam,S. and Lehnert,S.
TITLE Transcription profiling of cattle skin
JOURNAL Unpublished (2003)
COMMENT Contact: Dr Yonghong Wang
Functional Genomics Lab
CSIRO Livestock Industries
Level 5, Queensland Biosciences Precinct, University of Queensland,
306 Carmody Road St.Lucia QLD Australia
Tel: 07 3214 2445
Fax: 07 3214 2685
Email: Yonghong.Wang@csiro.au

```

```

FEATURES
source Plate: 25 row: B column: 04.
Location/Qualifiers
1..593
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Hereford Shorthorn"
/db_xref="taxon:9913"
/clone="CCL001471"
/sex="female"
/tissue_type="pooled"
/dev_stage="Adult"
/lab_host="XJ1-BlueMRP strain"
/clone_id="Bos taurus skin cDNA library"
/notes="Organ: skin; Vector: Uni-ZAPXR; Site 1: EcorI;
Site 2: Xho I; Library made from pooled skin of adult
female Hereford-Shorthorn."

```

ORIGIN

```

Alignment Scores:
Pred. No.: 4.15e-29 Length: 593
Score: 619.00 Matches: 105
Percent Similarity: 82.09% Conservative: 5
Best Local Similarity: 78.36% Mismatches: 24
Query Match: 76.61% Indels: 0
DB: Gaps: 0

```

US-09-994-365-2 (1-136) x CF765720 (1-593)

```

QY 3 LeuAsnTTrpLysLeuGlyTleuValLeuCySteuHisThrArgIYIleSerGly 22
Db 16 CTCACCTGGAACCTCTTAAGATCTGTCTTGTCTTGTCTGAGGATCTCAAGC 75
QY 23 SerGIuGlyHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThr 42
Db 76 AGAGAGACCAAGCTTCCCTCATCCAGAGAGATCTCAGAGAGAGAGGCGCTCCACCA 135
QY 43 LeuProGlnGlyProProValProGlyAspProTrpProGlyAlaProProLeuPheGlu 62
Db 136 TTGCTCAGGGGCCCCCAATCCTGTGTGACCCCTGGCCAGGGGCAACCCCGCTTGA 195
QY 63 AspProProProTrpArgProSerArgProTrpArgAspLeuProGluThrGlyValTrp 82
Db 196 GATCTCTCACTCCAGGCCCCCAATCGTCTCGAGAGACCTGCTGATTTGTGAGTCTGG 255
QY 83 ProProGluProProArgThrAspProProGlnProProArgProAspAspProTrpPro 102
Db 256 CCTCTGAACCCCTTAAGATGATCCCTCAACTCTCGGCTGAGACACCCCTGGCCC 315
QY 103 AlaGlyProGlnProProGluAsnProTrpProProAlaProGluValAspAsnArgPro 122
Db 316 GCAAGACCCCGAGCTCCAGAAACCCCTGGCCACCTGAGGTGAGACACGATCT 375
QY 123 GlnGluGluProAspLeuAspProProArgGluGluGlyTrpArg 136
Db 376 CACAGAGAGCCAGACCTTGACCCACCCAGGAGAGATACAGA 417

```

```

RESULT 3
AW315342 383 bp mRNA linear EST 09-JUL-2000
LOCUS AW315342
DEFINITION 12593 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION AW315342
VERSION AW315342.1 GI:6744598
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

```

```

REFERENCE
AUTHORS Fahrbrun,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R.,
Quackenbush,J., and Keele,J.W.
TITLE Porcine gene discovery by normalized cDNA-library sequencing and
EST cluster assembly

```

JOURNAL	Mamm. Genome 13 (8) , 475-478 (2002)
MEDLINE	22213789
PUBMED	12226715
COMMENT	Contact: Smith TPL

ORIGIN

Alignment Scores:

Pred. No.:	3,47e-29	Length:	383
Score:	617.00	Matches:	102
Percent Similarity:	85.83%	Conservative:	7
Best Local Similarity:	80.31%	Mismatches:	18
Query Match:	76.36%	Indels:	0
GB:	2	Gaps:	0

US-09-994-365-2 (1-136) X AW315342 (1-383)

QY	5	TRPLVSLenLEuGL1Y1LeuValLeuCYbLeuHLeThnArgGL1Y1LeSerGLYseRGLu	24
Db	3	TGGAAAGCTACTGGGGATCTGGTCTTTGCTCTTTGCGCGAGAGCATCTCAGGACAGCGGA	62
QY	25	GLYHISProSerHisAProProAlaGluAAsPArgGLuGLuAlaGlyeRProThrlLeuPro	44
Db	63	GACCAACCATCTCCCCCATCCACGAGAGGCTCAGAGAGAGAGGGCTCTCCACATTTGCTT	122
QY	45	GLInGlyProProValAProGLYAsPProTTPProGLYAlAProProLeuPheGLUAsPPro	64
Db	123	CGGGGCCCCCAATCCCCGGTAGCCTTTGGCCAGGGGGTACTCTCTATTCTTTGAGGACCCT	182
QY	65	ProProThnArgProSerArgProTTPArgAsPLeuProGLuThnGLYAlATTPProPro	84
Db	183	CCAGCTCCAGGGCCCAATGTCCTCTGGAGAGACTGCTCGAATCTGGAGCTTGGGCTCCTT	242
QY	85	GLUProProArgThnAsPProBProGLInProProArgProAsPAsPProTTPProAlaGLY	104
Db	243	GAACCCCTTAGTACTGATCCCCCTCAACCTCCCCGGGCTTGACGACACCCCTTGCCAGCAGGA	302
QY	105	ProGLInProProGLUAsPProTTPProProAlAProGLUValAsPAsnArgProGLInGLU	124
Db	303	CCCCAGCTCCAGAAACCCCTGGCCACTGCCCCCTGAGGTGGACACCGATCCCGAGAG	362
QY	125	GLUProAsPLeuAsPProPro	131
Db	363	GAGCCAGACTTTGACCCACCC	383

RESULT 4					
AI596929					
LOCUS	AI596929	422 bp	mRNA	linear	EST 21-APR-1995
DEFINITION	VJ4661.9.1 Strategene mouse skin (#937313)				Mus musculus cDNA clone
	IMAGE:932108 5', mRNA sequence.				

ACCESSION	AT596929	GI:460577
VERSION	AT596929.1	
KEYWORDS	BST.	
SOURCE	Mus musculus (house mouse)	

FEATURES

Source

```

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/cdb="IMAGE:932108"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clonelib="Stratagene mouse skin (#37313)"
/note="Organ: skin; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-AP XR Vector: ~5' adaptor sequence: 5' GAATTCGGCAGG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTT 3'"

```

US-09-994-365-2 (1-136) X AI596929 (1-422)

QY 11 IeuValLeuCYLeuH1aThrXArgLylLseG1seG1uG1uH1aProSerH1aPro 30
Db 2 CTGGCTCTTGCTGCTGTGCAAGAGGCAATTCAAGCAAT--GGCAACCTTCTCCCGA 58
QY 31 ProAlaGluAspArgGluGluLnaLag1YseProThrieuProGlnGlyProProValPro 50
Db 59 TCTACACACACCCAGAAAGGAGGACTCCCCACATTTGCTCTGGAGACCCCAATCTCT 118
QY 51 GlYAspProTrpProGlyValAProProLeuPheGluAspProProPheThrArgProSer 70
Db 119 GGGATCCCTGGCGCTGGGGCGGCTCTCTTTGTTATATGAACCTCGGCTCCAGGCTCCAA 178
QY ArgProTrpArgAspLeuProGluThrGlyValTyrProProGluProProArgThrAsp 90

Db	179	CGTCCCTGGAGAGATCTTCTCTGACAGAGTGTGCTGGCCCCCAAGGCCCAAGACACTGAT	238		
Qy	91	ProErgInProProArygProApsApsPProTrrProAlAgLyProGInProProGInUsn	110		
Db	239	CCCCCTAAACTCTCTGCTCGTAGTACCCTCTGGCCAGCAGAACCCCAAGAAAAC	298		
Qy	111	ProTrrProProAlaProGInUValApsApsApsPProGInGInGInProApsPLeuApsPro	130		
Db	299	CCCTGGGCTCTCTGGCCCCCTGAGATGAGCCATGATATCTCAGAGAGAGACCAGACTTGACCCA	358		
Qy	131	ProArygInGInUryAryg	136		
Db	359	CCCCAGAGAGAGCTATAGA	376		
RESULT 5					
AA530301		562 bp	mRNA	linear	EST 22-JUL-1997
LOCUS					
DEFINITION					
AA530301					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					
1					
2					
3					
4					
5					
6					
7					
8					
9					
10					
11					
12					
13					
14					
15					
16					
17					
18					
19					
20					
21					
22					
23					
24					
25					
26					
27					
28					
29					
30					
31					
32					
33					
34					
35					
36					
37					
38					
39					
40					
41					
42					
43					
44					
45					
46					
47					
48					
49					
50					
51					
52					
53					
54					
55					
56					
57					
58					
59					
60					
61					
62					
63					
64					
65					
66					
67					
68					
69					
70					
71					
72					
73					
74					
75					
76					
77					
78					
79					
80					
81					
82					
83					
84					
85					
86					
87					
88					
89					
90					
91					
92					
93					
94					
95					
96					
97					
98					
99					
100					
101					
102					
103					
104					
105					

	US-09-994-365-2(1-136) x AA530301 (1-562)
Oy	11 LeuValIeucYsleuHstIRrAgLYlleserGlyserLugluYHisProserHisPro 30
Db	1 CTGGTCTCTTGCCCTGTGTGCAGGAGGACATTTTCAGGCCAAT--GGCGACCCCTTCTCCCGGA 57
Oy	31 ProAlagluNspArggluGluluaIagLySerProThrneupProglngluYProProvalPro 50
Db	58 TCTACAGACACCACGAAAGAGAGACTCCCAACCATTTGGCTCTGGGACCCCAATCCT 117
Oy	51 GlysApPProTrpProglYlaIaProProleuPhegluAspProPProPProThraYProSer 70
Db	118 GGATATCCCTGGGCGCGGCCCTCTTTGTTGATCAACCTCCGCTCCAGGCTCCAAC 177
Oy	71 ArgProTrhpaNgaspleuProgluThrgluYalTrpProProgluPuProProxgThrasP 90
Db	178 CGTCCCTGGAGAGATCTTCTCGACAGTGGTGCTGGCCCCCAAGCCCCCAAGACTGAT 237
Oy	91 ProProgluInpProPratGrProaspPProTrpProAlagiYProginProProgluasn 110
Db	238 CCCCCTMAACCTCCTCGCTGATGACCCCTGGCACAGGACCCAGCCCCCGAGAACAAC 297
Oy	111 ProTrpProProAlaIaProgluValaIsPaasnArYProglngluYluProaspLeuaspPro 130
Db	298 CCTGGGCTCTGCGCCCTGAGATGACCATGAATCTCAGAGAGAGCCAGACTTGACCCA 357
Oy	131 ProArggluYluYTrArG 136
Db	358 ACCCAGAGAGATTAAGA 375
RESULT 6	
CG484009	451 bp DNA linear GSS 01-OCT-2003
LOCUS	OST17807 Mus musculus 129Sv/Ev Mus musculus genomic clone OST17807,
DEFINITION	genomic survey sequence.
ACCESSION	CG484009
VERSION	CG484009.1 GI:37239343
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 451) Zambrowicz,B.P., Abidin,A., Ramirez-Solis,R., Richter,L.U., Pisgott,J., BeltrandeRio,H., Buxton,E.C., Edwards,U., Finch,R.A., Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W., Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparkes,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N., Zhao,Q., Person,C., and Sands,A.T. mml kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003) Contact: Zambrowicz BP
TITLE	OmiBank
JOURNAL	Lexicon Genetics Incorporated 4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: maternal@lexgen.com Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)
COMMENT	Class: Gene Trap Location/Qualifiers 1..451 /organism="Mus musculus" /mol_type="genomic DNA" /strain="129Sv/Ev" /db_xref="taxon:10090" /clone="OST17807" /cell_type="embryonic stem cell" /clone_id="Mus musculus 129Sv/Ev"
FEATURES	
source	
ORIGIN	

Alignment Scores:

Pred. No.:	1.57e-22	Length:	451
Score:	510.50	Matches:	83
Percent Similarity:	82.05%	Conservative:	13
Best Local Similarity:	70.94%	Mismatches:	20
Query Match:	63.18%	Indels:	1
DB:	9	Gaps:	1

US-09-994-365-2 (1-136) x CG484009 (1-451)

QY 20 TleserGlyserGluGlyHisProSerHisProAlaGluAspArgGluGluAlaGly 39
 DB 3 ATTTTCAGGCAAT---GGCGACCCCTTCTCCCGATCTACAGACACCCAGAGAGAGAGAC 59

QY 40 SerProThrLeuPProGlnGlyProProValProGlyAspProTTPProGlyAlaProPro 59
 DB 60 TCCCGACATTGCTCTGGGACCCCGCAATCCCTGTATCTCTGCGGCGGCGCTCTCT 119

QY 60 LeupheGluAspProProProProThraArgProSerArgProTTPAAspLeuProGluThr 79
 DB 120 TTGTTTATGAACTCCGCGCTCCAGGCTCCAGCTCCCTGAGATCTTCTTGACACT 179

QY 80 G1yValTrpProGluProProArgThraAspProGlnProProArgProAspAsp 99
 DB 180 GGTGCTGCGCCCGCAAGACCCCGCAAGCACTGATCCCTTAACTCTCTGCTGATGAC 239

QY 100 ProTTPProAlaGlyProGlnProProGluAspProTTPProProAlaProGluValAsp 119
 DB 240 CCGTGGCGACAGAGACCCCGCAAGAAACCCCTGCGCTCTGCGCTGAGATGAGC 299

QY 120 AsnArgProGlnGluGluProAspLeuAspProProArgGluGluTrpArg 136
 DB 300 CATGAATCTCAGAGAGAGACCACTTGACCCACCCAGAGAGATAGA 350

RESULT 7
 CG481452 416 bp DNA linear GSS 01-OCT-2003
 LOCUS OST13885 Mus musculus 1295v/Ev Mus musculus genomic clone OST13885,
 DEFINITION genomic survey sequence.
 ACCESSION CG481452
 VERSION CG481452.1 GI:37233834
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 AUTHORS 1 (bases 1 to 416)
 Zambrwitz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
 Piggott,J., Beltranderio,H., Buxton,B.C., Edwards,J., Finch,R.A.,
 Fiddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaiing,C.,
 Key,B.W., Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
 Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
 Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
 Zhu,Q., Person,C. and Sands,A.T.
 Mkl kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 CONTACT: Zambrwitz BP
 OMNIBANK
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrwitz et al (Nature. 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap.
 Location/Qualifiers
 1..416
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST13885"
 /cell_type="embryonic stem cell"

ORIGIN /clone_1ib="Mus musculus 1295v/Ev"

Alignment Scores:

Pred. No.:	2.37e-22	Length:	416
Score:	507.00	Matches:	80
Percent Similarity:	82.14%	Conservative:	12
Best Local Similarity:	71.43%	Mismatches:	20
Query Match:	62.75%	Indels:	0
DB:	9	Gaps:	0

US-09-994-365-2 (1-136) x CG481452 (1-416)

QY 25 G1yHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThrLeuPro 44
 DB 14 GGGACCCCTTCTTCCGATCTACAGACACCCAGAGAGAGACTCCACCATTCCT 73

QY 45 GlnGlyProProValProGlyAspProTTPProGlyAlaProProLeupheGluAspPro 64
 DB 74 CTGGACCCCGCAATCCCTGTGATCCCTGCGCTGGGCGGCGCTCTTGTGATGAACT 133

QY 65 ProProThraArgProSerArgProTTPAAspLeuProGluThrGlyValTTPProPro 84
 DB 134 CCGCTTCAAGCTCCAGACCCCTGAGAGATCTTCTTCAAGAGTGTGCTGCGCCCA 193

QY 85 GluProProArgThraAspProProGlnProProArgProAspAspProTTPProAlaGly 104
 DB 194 AAGCCCCAGACATGATCCCTTAACTCTCTGCTGATGACCTTGGCGAGAG 253

QY 105 ProGlnProProGluAspProTTPProProAlaProGluValAspAspArgProGlnGlu 124
 DB 254 ACCAGCCCCAGAAACCCCTGCGCTCTGCGCTGAGATGAGCATGATCTCAGAG 313

QY 125 GluProAspLeuAspProProArgGluGluTrpArg 136
 DB 314 GAGCGACACCTTGACCCACCCAGAGAGATAGA 349

RESULT 8
 CG484609 669 bp DNA linear GSS 01-OCT-2003
 LOCUS OST18617 Mus musculus 1295v/Ev Mus musculus genomic clone OST18617,
 DEFINITION genomic survey sequence.
 ACCESSION CG484609
 VERSION CG484609.1 GI:37240590
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 AUTHORS 1 (bases 1 to 669)
 Zambrwitz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
 Piggott,J., Beltranderio,H., Buxton,B.C., Edwards,J., Finch,R.A.,
 Fiddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaiing,C.,
 Key,B.W., Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
 Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
 Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
 Zhu,Q., Person,C. and Sands,A.T.
 Mkl kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 CONTACT: Zambrwitz BP
 OMNIBANK
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrwitz et al (Nature. 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap.
 Location/Qualifiers
 1..669
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="129Sv/Ev"

```

/db_xref="taxon:10090"
/clone="OST18617"
/cell_type="embryonic stem cell"
/clone_1fb="Mus musculus 129Sv/Ev"

```

Alignment Scores:	
Pred. No.:	4,52e-22
Score:	506.00
Percent Similarity:	82.14%
Best Local Similarity:	71.43%
Query Match:	62.62%
DB:	
CG484609 (1-669)	
Length:	669
Matches:	80
Conservative:	12
Mismatches:	20
Indels:	0
Gaps:	0

Qy 25 G L Y H I S P R O S E R H I S P R o P r o a l a e l u s p a r g i n g u l a l a g l y S e r P r o t h r e u P r o 44
Db 8 G G C A C C T T T C T C C C G G A T C T A C A C A C C C A G A A G G A G A C T C C C C A C C A T T G C T 67
Qy 45 G l n g l y P r o P r o V a l P r o G l y A s p P r o T r p P r o G l y A l a P r o P r o l e u P h e G l u s P r o 64
Db 68 C T G G A C C C C A A T C C T G T G A T C C T G G C C T G G G C G C C T C T T T G T T A T A G A C C T 127
Qy 65 P r o P r o T h r A r g P r o S e r A r g P r o T r p A r g A s p L e u P r o G l u T h r G l y V a l T r p P r o P r o 84
Db 128 C C G C C T C A G G C T C C A C C G T C C T G G A G A G A T C T T C T G A C A G T G T C C T G G C C C C A 187
Qy 85 G l u P r o P r o A r g T h r A s p P r o P r o G l n P r o P r o A r g P r o A s p A s p P r o T r p P r o a l a g l y 104
Db 188 A A G C C C C A A C A C T G A T C C C C T A A C C T C C T G C C G A T A G A C C C C T G G C A G A G A 247
Qy 105 P r o G l n P r o P r o G l u A s n P r o T r p P r o P r o A l a P r o G l u V a l A s p A s n A r g P r o G l n g l u 124
Db 248 A C C C A G C C C C A G A A A A C C C C T G G C T C T G C C C C T G A A T G A C C A T A A T C T C A G A G 307
Qy 125 G l u P r o A s p L e u A s p P r o P r o A r g G l n g l u T y r A r g 136
Db 308 G A G C C A G A C C T T T G A C C C A C C C C A G A A G A G T A A G A 343

LOCUS	CG487403	442 bp	DNA	linear	GSS 01-OCT-2003
DEFINITION	OSR22893	Mus musculus	129Sv/Ev	Mus musculus genomic clone	OSR22893,
ACCESSION	CG487403				
VERSION	CG487403.1	GI:37246315			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus. 1 (bases 1 to 442)				
AUTHORS	Zambrowicz, B. P., Abuin, A., Ramirez-Solis, R., Richter, L. J., Piggett, J., Beltrandeliro, H., Buxton, E. C., Edwards, J., Finch, R. A., Fiddle, C. J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jais, C., Key, B. W., Jr., Kipp, P., Konhaff, B., Ma, Z. Q., Makseich, D., Payne, R., Potter, D. G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M. J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A. T.				
TITLE	Mtl1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)				
COMMENT	Contact: Zambrowicz BP				

Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: material@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers
1..442
source

```

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST32893"
/cell_type="embryonic stem cell"
/clone_idb="Mus musculus 129Sv/Ev"

```

Alignment Scores:	
Pred. No.:	5.93e-22
Score:	501.00
Percent Similarity:	82.73%
Best local Similarity:	71.82%
Query Match:	62.00%
DB:	9
Length:	442
Matches:	79
Conservative:	12
Mismatches:	19
Indels:	0
Gaps:	0

US-09-994-365-2 (1-136) x CG487403 (1-442)

Qy 27 ProSezhiarProAlaGluAspArgGluGluAlaGlySerProThiLeuProGlnGly 46
Db 4 CTTTCTCCGGATCTAAGACACCCACGAAAGAGGAGACTCCACCATTTGCTCTGGGA 63

Qy 47 ProProValProGlyAspProThrProGlyAlaProValLeuProGluProGluAspProProPro 66
Db 64 CCCCACATCCCTGGAGATCCCTGGCTGGGGGCGCTCTTTGTTGATGAACCTCGCCT 123

Qy 67 ThrArgProSerArgProThrArgAspLeuProGluThiGlyAlaTTPProProGluPro 86
Db 124 CCAAGGCTCCAAACGCTCCCGAGAGAAATTCTCTACAGTGTGCTGGCCCCAAAGCC 183

Qy 87 ProArgThrAspProGlnProGlnProArgProAspAspProTTPProAlaGlyProGln 106
Db 184 CCAAGCACTGATCCGCCCTAAACCTCTGCTGCTGATGACCTCTGGCAGAGAAACCCAG 243

Qy 107 ProProGluAsnProTTPProProProAlaProGluValaAspAsnAspProGlnGluGluPro 126
Db 244 CCCCCGAAAAACCCCTGGCTCTGCCCCCTGAGATGACCATTAATCTCGAGAGAGACCA 303

Qy 127 AspLeuAspProProArgGluGluGlyArg 136
Db 304 GACCTTGACCCACCCCAAGAAAGATGTGA 333

RESULT	10
LOCUS	CG473878
DEFINITION	CG473878 475 bp DNA linear GSS 01-OCT-2003 OST1668 Mus musculus 129Sv/Ev Mus musculus genomic clone OST1668,
ACCESSION	CG473878
VERSION	CG473878.1 GI:37224767
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionath; Muridae; Murinae; Mus. 1 (bases 1 to 475)
AUTHORS	Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richer,J.J., Piggott,C.J., Belrandel,Rio,H., Buxton,B.C., Edwards,J., Finch,R.A., Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jang,C., Key,B.W., Jr., Kipp,P., Konlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Speake,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.
TITLE	Mhl kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT	Contact: Zambrowicz BP

Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature, 1998 Apr 9;352(6676):1608-11)

Class: Gene Trap.
Location/Qualifiers
1. 475
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OSR1668"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Alignment Scores:
Pred. No.: 4.25e-20 Length: 475
Score: 471.50 Matches: 74
Percent Similarity: 80.37% Conservative: 12
Best Local Similarity: 69.16% Mismatches: 16
Query Match: 58.35% Indels: 5
Gaps: 1

US-09-994-365-2 (1-136) x CG473878 (1-475)

QY 29 HisProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGlyProPro 48
Db 40 CACCCA-----CGAAAGAGAGATCCCAACCATTCCTCTGGAGACCCCA 84

QY 49 ValProGluAspProTTPProGluValaProLeuPheGluAspProProProThrArg 68
Db 85 ATCCCTGGTATCCCTGGAGGAGCTCTGCTGTTGTTGTAAGACCTCCCTCCAGGC 144

QY 69 ProSerArgProTTPArgAspLeuProGluThrGlyValTTPProProGluProProArg 88
Db 145 TCACACGCTCTCGAGAGATCTTCTGACAGTGTGCTGCTGCCCCCAAGCCCAAGC 204

QY 89 ThrAspProProGluProProArgProAspAspProTTPProAlaGlyProGlnProPro 108
Db 205 ACTGATCCCTCTAAACCTCTCTGCTGATGACCTGCTGACAGAGAGAACCCAGCCCA 264

QY 109 GluAsnProTTPProProAlaProGluValaAspAsnArgProGlnGluProAspLeu 128
Db 265 NAAAGCCCTGCTGCTCTGCTGCTGAAATGAGACCATGATCTCAGAGAGCCANACCTT 324

QY 129 AspProProArgGluGluTyr 135
Db 325 GACCCACCCCAAGAAATAT 345

RESULT 11
CG474695 322 bp DNA linear GSS 01-OCT-2003
LOCUS OST2738 Mus musculus 129Sv/Ev Mus musculus genomic clone OST2738,
DEFINITION genomic survey sequence.
ACCESSION CG474695
VERSION CG474695.1 GI:37225584
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 322)
REFERENCE
AUTHORS Zambronicz, B.P., Abidin, A., Ramirez-Solis, R., Richter, L.J.,
Pisgott, D., Beltranderio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jasing, C.,
Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Spark, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C. and Sands, A.T.
Wnt1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
CONTACT: Zambronicz BP
OmitBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: material@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambronicz et al (Nature, 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers
1. 322
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST2738"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Alignment Scores:
Pred. No.: 1.45e-19 Length: 322
Score: 460.00 Matches: 74
Percent Similarity: 82.35% Conservative: 10
Best Local Similarity: 72.55% Mismatches: 17
Query Match: 56.93% Indels: 1
Gaps: 0

US-09-994-365-2 (1-136) x CG474695 (1-322)

QY 36 GluGluAlaGlySerProThrLeuProGlnGlyProProValProGlyAspProTTPPro 55
Db 6 AAAGAGAGAGACCTCCCAACCATTCCTGAGACCCCAATCCCTGATCCCTGAGCT 65

QY 56 GluAlaProProLeuPheGluAspProProProThrArgProSerArgProTTPArgAsp 75
Db 66 GGGGCGCTCTCTTGTGTTGTAAGACCTCCGCTCAGAGCTCAACCGTCCCTGAGAGAT 125

QY 76 LeuProGluThrGlyValTTPProProGluProProArgThrArgProProProGlnProPro 95
Db 126 CTTCCTGACNTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 185

QY 96 ArgProAspAspProTTPProAlaGlyProGlnProProGluAsnProTTPProProAla 115
Db 186 CTGCTGATGACCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 245

QY 116 ProGluValaAspAsnArgProGlnGluProAspLeuAspProProArgGluGluTyr 135
Db 246 CTTGAGATGAGCCTGATGATCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 305

QY 135 TAGT 136
Db 306 TAGA 309

RESULT 12
AA763309 332 bp mRNA linear EST 27-JAN-1998
LOCUS v069h03.r1 StrataGene mouse skin (#537313) Mus musculus cDNA clone
DEFINITION IMAGE:1229621 5', mRNA sequence.
ACCESSION AA763309
VERSION AA763309.1 GI:2813056
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 332)
REFERENCE
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucada, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theisinger, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
CONTACT: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LML; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:655213

Seq primer: -28m13 rev1 ET from Amersham
 High quality sequence stop: 329.

FEATURES

SOURCE

1. .332
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:1229621"
 /sex="females"
 /tissue_type="whole skin"
 /dev_stage="11 weeks old"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene mouse skin (#937313)"
 /note="Organ: skin; Vector: phage-script SK; Site: 1:
 EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
 Oligo dt. Whole skin from 11 week old C57BL/6 female mice.
 Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
 adaptor sequence: 5' GAATTCGGCAGAG 3' ~3' adaptor
 sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

ORIGIN

Alignment Scores:

Pred. No.: 1.02e-18 Length: 332
 Score: 446.50 Matches: 77
 Percent Similarity: 81.48% Conservative: 11
 Best Local Similarity: 71.30% Mismatches: 15
 Query Match: 55.26% Indels: 7
 DB: 1 Gaps: 1

US-09-994-365-2 (1-136) x AA763309 (1-332)

Qy 29 HisProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGlyProPro 48
 Db 3 CACCCA-----GGAAGAGAGAGACTCCACCATTCCTCTGGAGACCCCA 47
 Qy 49 ValProGluAspProTrpProGluYAlaProProLeuPheGluAspProProProThaArg 68
 Db 48 ATCCCTGGTGAATCCCTGGCCCTGGGGG-CCTCCTTTGTTGATGAACCTCCGCTCC-AGG 105
 Qy 69 ProSerArgProTrpArgAspLeuProGluThrglyValTTPProProGluProProArg 88
 Db 106 TCCAAACCTCCCTGGAGAGATCTCTCTGACAGTGTGCTGCCCCCAAAACCCCAAGC 165
 Qy 89 ThrAspProProGlnProProArgProAspAspProTrpProAlaGlyProGlnProPro 108
 Db 166 ACTGATCCCCCTAAACCTCTCTGCTGATATACCCCTGCAAGAGAACCAAGCCCA 225
 Qy 109 GluAsnProTrpProProAlaProGluValAspAsnArgProGlnGluGluProAspLeu 128
 Db 226 GAAACCCCTGGCCCTCCGCCCCCTGAGATGACCATGATCTCAGAGAGACCAAGACTT 285
 Qy 129 AspProProArgGluGluTyrArg 136
 Db 286 GACCAACCCCAAGAGAGATATAGA 309

RESULT 13

CG474680

LOCUS CG474680 386 bp DNA linear GSS 01-OCT-2003
 DEFINITION OST2720 Mus musculus 129Sv/Ev Mus musculus genomic clone OST2720,
 genomic survey sequence.

ACCESSION

CG474680

VERSION CG474680.1 GI:37225569
 KEYWORDS GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (Pages 1 to 386)
 Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
 Piggett, J., Beltrande-Rico, H., Buxton, E.C., Edwards, J., Finch, R.A.,
 Fridele, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaring, C.,
 Key, B.W., Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,
 Payne, R., Potter, D.G., Qian, N., Shaw, J., Schlick, J., Shi, Z.-Z.,
 Spark, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
 Zhu, Q., Person, C. and Sands, A.T.
 Mki kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 Contact: Zambrowicz BP
 OmniBank

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

1. .386
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST2720"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Alignment Scores:

Pred. No.: 2.61e-18 Length: 386
 Score: 441.00 Matches: 68
 Percent Similarity: 75.45% Conservative: 15
 Best Local Similarity: 61.82% Mismatches: 27
 Query Match: 54.58% Indels: 0
 DB: 9 Gaps: 0

US-09-994-365-2 (1-136) x CG474680 (1-386)

Qy 27 ProSerHisProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGly 46
 Db 7 CCTTCTCCCGAGATCTACAGACCCCAAAAAGAGAGACTCCACCATTCCTCTGGGA 66
 Qy 47 ProProValProGluAspProTrpProGluYAlaProProLeuPheGluAspProProPro 66
 Db 67 CCCCAGATCCCTGGTGAATCCCTGGCCCTGGGGGCGCTCTTTGTTGATGAACCTCCGCT 126
 Qy 67 ThrArgProSerArgProTrpArgAspLeuProGluThrglyValTTPProProGluPro 86
 Db 127 CCAAGCTCAACCGTCCCTGGANAGATCTCTGACANTGTGCTGCGCCCAAGCCC 186
 Qy 87 ProArgThrAspProProGlnProProArgProAspAspProTrpProAlaGlyProGln 106
 Db 187 CCNAGCCTGATCCCTCTAAACCTCTGCTGCTGATNAACCCCTGGCAGAGAACCCAN 246
 Qy 107 ProProGluAsnProTrpProProAlaProGluValAspAsnArgProGlnGluGluPro 126
 Db 247 CCCCAGAAAACCCCTGGCCCTCTGCCCCCTGAATGACATGATCTCAGAGAGACCA 306
 Qy 127 AspLeuAspProProArgGluGluTyrArg 136
 Db 307 AACCTGACCCNCCCAAGAAATATATAA 336

RESULT 14

AA798896

LOCUS AA798896 451 bp mRNA linear EST 10-FEB-1998
 DEFINITION vv94e08.f1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
 IMAGE:1230086 5', mRNA sequence.

ACCESSION

AA798896

VERSION AA798896.1 GI:2861851
 KEYWORDS EST.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 451)
AUTHORS Maira,M., Hallier,L., Allen,M., Bowles,M., Dietrich,N., Dubouche,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Stepien,M., Tan,F., Underwood,K., Moore,B., Weisberg,B., Wyle,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The Washu-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Maira M/Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
MG1:655678
Putative full length read
vector to vector length is 671
Seq primer: -28m13 rev1 EF from Amersham
High quality sequence stop: 431.
Location/Qualifiers
1..451
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1230086"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse skin (#937313)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1: EcorI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'"

ORIGIN
Alignment Scores:
Pred. No.: 3e-17 Length: 451
Score: 425.00 Matches: 71
Percent Similarity: 89.01% Conservative: 10
Best Local Similarity: 78.02% Mismatches: 10
Query Match: 52.60% Indels: 2
DB: 1 Gaps: 0

US-09-994-365-2 (1-136) x AA798896 (1-451)
QY 46 G1YProProValPProG1YAspProTTPProG1YAlaPProPoleuPheGluAspProPro 65
DB 1 GGACCCCAACCTCTGGATCCCTGGCTGCGGAGG-CCTCTTTGTTTGAAGAACCTCCG 59
QY 66 ProThrArgProSerArgProTTPArgAspLeuProGluTyrGluValTTPProProGlu 85
DB 60 CTCACAGCTCAAC-CGTCCCTGGAGAGATCTCTCTGACAGTGGAGCTGGCCCCCAAG 118
QY 86 ProProArgTThrAspProG1YAspProTTPProArgProAspAspProTTPProAlaG1YPro 105
DB 119 CCCCCAAGCACTGATCCCTTAAACCTCTCGCTGATGACCTTGGCCGACGAGAAC 178
QY 106 G1nProProGluAsnProTTPProProAlaPProG1YValAspAsnArgProG1nGlu 125
DB 179 CAGCCCCCAAGAAACCTCTGGCTCTGCCCCCTGAGATGACATGATCTCAGAGAG 238
QY 126 ProAspLeuAspProProArgG1nGluTyrArg 136

DB 239 CCAGCCTTGACCAACCCAGAGAGATATGA 271
RESULT 15
LOCUS CG528207 395 bp DNA linear GSS 01-OCT-2003
DEFINITION OSR107284 Mus musculus 129SV/Bv Mus musculus genomic clone
ACCESSION CG528207
VERSION CG528207.1 GI:37314779
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 395)
AUTHORS Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Piggett,J., Beltrando,Rio,H., Buxton,E.C., Edwards,J., Finch,R.A., Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaiing,C., Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.
TITLE Wnt1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: material@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers
1..395
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129SV/Bv"
/db_xref="taxon:10090"
/clone="OSR107284"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129SV/Bv"

ORIGIN
Alignment Scores:
Pred. No.: 3.2e-14 Length: 395
Score: 375.00 Matches: 63
Percent Similarity: 79.57% Conservative: 11
Best Local Similarity: 67.74% Mismatches: 17
Query Match: 46.41% Indels: 2
DB: 9 Gaps: 0

US-09-994-365-2 (1-136) x CG528207 (1-395)
QY 46 G1YProProValPProG1YAspProTTPProG1YAlaPProPoleuPheGluAspProPr 65
DB 3 GGACCCCAACCTCTGGATCCCTGGCTGCGGAGGCTCTTGTGTAAGAACCTNC 62
QY 65 oProThrArgProSerArgProTTPArgAspLeuProG1YValTTPProProG1 85
DB 63 GCTTNCAGGCTTCAACCTCTGAGATNTTTCAGACGTGTGCTGCCCCCAA 122
QY 85 uProProArgTThrAspProProG1nProProArgProAspAspProTTPProAlaG1Y 105
DB 123 GCCCCAAGCACTGATCCCTTAAACCTTCTGCTGATGACCTTGGCCGACAGAA 182
QY 105 roG1nProProGluAsnProTTPProProAlaPProG1YValAspAsnArgProG1nGlu 125
DB 183 CCGAGCCCCCAAGAAACCTCTGCTTNNTGCCCTGAGATGACATGATCTCAGAGAG 242
QY 125 1uProAspLeuAspProProArgG1nGluTyrArg 136

Thu Jan 13 09:19:07 2005

us-09-994-365-2.p2n.rst

Page 10

Db 243 AGCCAGACCTTGACCCACCCAGAGAGTATAGA 277

Search completed: January 11, 2005, 19:52:35
Job time : 2829.18 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 12, 2005, 16:40:28 ; Search time 83 Seconds
(without alignments)
976.264 Million cell updates/sec

Title: US-09-994-365-3
Perfect score: 692
Sequence: 1 SEGHPSHPAEDREAGSPF.....EVDNRPOEBDLPPEEYR 114

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 824507 seqs, 355394441 residues
Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DRV=x1h
-Q=/cgn2_1/USFTO_spool_h/US0994365/runat_12012005_164014_11183/app_query.fasta_1.263
-DB=Issued_Patents_NA -OPMT=fastap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bl0sum62 -TRANS=human40.cdt
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NODM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0994365 @CGN 1.1 69 @runat_12012005_164014_11183 -NCPU=6 -ICPI=3
-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFBLOCK=100 -LONGCLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*
1: /cgn2_6/prodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCtus.COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	304.5	44.0	248	3	US-09-621-976-9776
C 2	198.5	28.7	4403765	3	US-09-103-840A-1
C 3	198.5	28.7	4411529	3	US-09-103-840A-1
C 4	190.5	27.5	1926	4	US-09-249-585A-4
C 5	190.5	27.5	1931	2	US-09-130-114-2
C 6	188.5	27.2	4403765	3	US-09-103-840A-2
C 7	188.5	27.2	4403765	3	US-09-103-840A-2
C 8	182	26.3	114793	4	US-10-148-806-3
C 9	181	26.2	6530	2	US-08-146-930-1
C 10	181	26.2	6530	2	US-08-146-930-1
C 11	181	26.2	6530	5	PCT-US93-03993-1
C 12	180.5	26.1	1854	4	US-09-894-844-103

C 13	180	26.0	1280	3	US-09-060-756-4	Sequence 4, Appli
C 14	180	26.0	1280	4	US-09-670-314-4	Sequence 4, Appli
C 15	179.5	25.9	15231	3	US-09-128-155-16	Sequence 16, Appli
C 16	176	25.4	320	3	US-09-165-264-14	Sequence 14, Appli
C 17	174.5	25.2	2830	2	US-09-010-9288-1	Sequence 1, Appli
C 18	171.5	24.8	1173	4	US-09-894-844-60	Sequence 60, Appli
C 19	171	24.7	320	3	US-09-165-264-7	Sequence 7, Appli
C 20	171	24.7	320	3	US-09-165-264-11	Sequence 11, Appli
C 21	171	24.7	1926	4	US-09-249-585A-2	Sequence 2, Appli
C 22	171	24.7	1926	4	US-09-410-399-3	Sequence 3, Appli
C 23	171	24.7	2580	3	US-09-050-863-2	Sequence 2, Appli
C 24	171	24.7	2580	3	US-09-359-081-2	Sequence 2, Appli
C 25	171	24.7	5452	2	US-09-130-114-1	Sequence 1, Appli
C 26	171	24.7	8705	4	US-09-647-344A-14	Sequence 14, Appli
C 27	171	24.7	9600	4	US-09-910-647-1	Sequence 1, Appli
C 28	171	24.7	9600	4	US-09-620-925-1	Sequence 1, Appli
C 29	171	24.7	10596	1	US-07-884-811-15	Sequence 15, Appli
C 30	171	24.7	10596	1	US-07-885-971-15	Sequence 15, Appli
C 31	171	24.7	10596	1	US-08-087-783A-15	Sequence 15, Appli
C 32	171	24.7	10596	1	US-08-194-088B-15	Sequence 15, Appli
C 33	171	24.7	10596	2	US-08-194-087-15	Sequence 15, Appli
C 34	171	24.7	10596	5	PCT-US93-04648-15	Sequence 15, Appli
C 35	171	24.7	16080	4	US-09-724-566A-48	Sequence 48, Appli
C 36	170	24.6	318	3	US-09-165-264-12	Sequence 12, Appli
C 37	169.5	24.5	320	3	US-09-165-264-13	Sequence 13, Appli
C 38	169	24.4	290	3	US-08-818-112-37	Sequence 37, Appli
C 39	169	24.4	290	3	US-08-818-112-37	Sequence 37, Appli
C 40	169	24.4	290	3	US-09-056-556-37	Sequence 37, Appli
C 41	169	24.4	290	4	US-09-072-596-37	Sequence 37, Appli
C 42	169	24.4	290	4	US-09-072-597-37	Sequence 37, Appli
C 43	168.5	24.3	1548	2	US-08-762-106-5	Sequence 5, Appli
C 44	168.5	24.3	1548	3	US-09-320-774-5	Sequence 5, Appli
C 45	168.5	24.3	1581	2	US-08-762-106-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-621-976-9776/c
Sequence 9776, Application US/09621976
Patent NO. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Giordano, J.Y.
TITLE OR INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 9776
LENGTH: 248
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 188
OTHER INFORMATION: n=a, g, c or t
US-09-621-976-9776

Alignment Scores:
Pred. No.: 7.25e-13
Score: 304.50
Percent Similarity: 88.33%
Best Local Similarity: 86.67%
Query Match: 44.00%
DB: 4
Gaps: 1
US-09-994-365-3 (1-114) x US-09-621-976-9776 (1-248)

QY 56 GUAThrcGlyValTrpProGluProGlyArgThrAspProGlnProArgPro 75
|||||

[illegible]

```

QY      83 -----ProGlnPProGluAaMProTTrpProProLaProGluValaAspAnaArg 99
Db      1091065 CCGGAAGCCCCCAACTCCGGCGAGACCACTTGCGGCCGCACACACCGTTG----- 1091015

QY      100 ProGlnGluInUProAspLeuAspPro 108
Db      1091014 CCGAAATGACAGCCCGCGCTTGCCGCCG 1090988

RESULT 3
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.:          0.143           Length:         4411529
Score:             198.50           Matches:        51
Percent Similarity: 32.54%           Conservative:   4
Best Local Similarity: 30.18%           Mismatches:    45
Query Match:       28.68%           Indels:        69
DB:                  3                Gaps:          6

US-09-994-365-3 (1-114) x US-09-103-840A-1 (1-4411529)

QY      5 ProSerHisProProAlaGluAspArgylGluAlaGlySerProThrLeuProGlnGly 24
Db      1091485 CCGCGCATGCGCGCCGCGCGCGCGCTGCGCCGCGCGCTGCGCGCGCGCCGACAACGCCG 1091426

QY      25 ProProvalaProGlyAspProTTrpProGlyAlaProProleuheGluAspPro----- 42
Db      1091425 CCACCTACCGCGCGCGCGCCTTGCGCGCGGTGCGCGCGCACACCAGCACCCTGCGCTG 1091366

QY      43 -----ProProThraArgProSerArg 49
Db      1091365 CCGCGCATCCACCCGCGCGAACACACGATCCCGCGCGCGCGCGCGCTGCCCGCGCG 1091306

QY      50 ProTrp-----ArgAspLeuPro 55
Db      1091305 CCCCTGCGCGCGCTTGCTGCACAAATGCGACCGGTATGCTTCAGCGCGCCAGCGCGTGC 1091246

QY      56 GluThrGlyValaTTrpProProGluProProArgThraSp----- 68
Db      1091245 CGACGACCGCGCTTGCCACCAATGCCGCGGTACCGGCATGCGCGGTGATTCCCCTGTG 1091186

QY      69 -----ProProGlnPro 72
Db      1091185 CCGAAACAACGCGCGAGCGGTGGCGCGACCCCGCGCGCGCGCGCGAATGCGCGCATGCCC 1091126

QY      73 ProArgProAspAspProTTrpProAlaGly----- 82
Db      1091125 CCGATGCGCGCGCGGTGCGG-----CCGCGCGAGAACCGACACCATGCGCGCGCGCGCTCCG 1091069

QY      83 -----ProGlnPProGluAaMProTTrpProProLaProGluValaAspAnaArg 99
Db      1091068 CCGGAAGCCCCCAACTCCGGCGAGACCACTTGCGGCCGCACACCGTTG----- 1091018

```



```

QY      43  ProProthruAArgProSeraArgProTrrPArgAspleuProbiUnhrGlyValTrrProPro  62
          |||||
Db       82649  CCACCAACCAACCACTCCACCAACA-----CCACCA  82678
          |||||

QY      63  GluProPoaAgnThraAPProProGlnInProPoaArgProAAspAPProTrrProAagly  82
          |||||
Db       82679  CCACCACTCTCCACCAACCAACCAACCAACCACTCTCCACCAACCACTCTCCACCA  82738
          |||||

QY      83  ProGlnInProPoaGluAAnProTrrProProAlaAPProGluValAspAAnArgProGlnGlu  102
          |||||
Db       82739  CCTCCACTCTCCACCAACCAACCACTCTCCACCACTCTCCACCACTCTCCACCACTCTCCACCA  82798
          |||||

QY      103  GluProAAspleuAAspProPro  109
          |||||
Db       82799  CCACCACTCTCCACCAACCAACA  82819
          |||||

RESULT 9
US-08-146-930-1/c
Sequence 1, Application US/08146930
Patent No. 5958764
GENERAL INFORMATION:
APPLICANT: Roop, Dennis R.
APPLICANT: Rothnagel, Joseph A.
APPLICANT: Greenhalgh, David A.
TITLE OF INVENTION: SPECIFIC EXPRESSION VECTORS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,930
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: two
APPLICATION NUMBER: 07/876,266
FILING DATE: April 30, 1992
APPLICATION NUMBER: No. 5958764 yet assigned (204/132)
FILING DATE: October 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 204/152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6530 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-146-930-1

Alignment Scores:
Pred. No.: 0.0028 Length: 6530
Score: 181.00 Matches: 50
Percent Similarity: 39.60% Conservative: 46
Best Local Similarity: 33.56% Mismatches: 46
Query Match: 26.16% Indels: 44

```

```

DB: 2 Gaps: 6
US-09-994-365-3 (1-114) x US-08-146-930-1 (1-6530)
QY 8 ProProAlaGluAaPArgGluGluAlaGlySerProThrLeu----- 21
Db 4081 CCACCTCCAGAGCCGCCACCAAGAGAGCGCGCTCCGACGCTGGAGCCACCGCTCCGCT 4022
QY 22 -----ProGInGlyProProVal---ProGlyAaPProTrrProGlyAla 35
Db 4021 CCGAGTAGACTCTCTCCGACAGCCACCGCGCTGCTCCGAAAGACCACTCCGACGCCA 3962
QY 36 ProProLeu---PheGluAaPProProProThrArgProSerAArgProTrrPArgAAspleu 54
Db 3961 CCGCGCGCTCCCGCCGAAAGAGCCCGCCGCAAGCCACCGCTCCGAGTAGAAGCTTCA 3902
QY 55 ProGluThrGlyValTrrProProGluAaPProBrrArgThraaPProProGInProProArg 74
Db 3901 CCGGACGACCGCGCTGCTGCGCCACCAACCGCTGAAGTAGACAGCCACCGCGCACCGCG 3842
QY 75 ProAaPAppProTrrProAlaGlyProGInProBrrGluAaPPro----- 89
Db 3841 CCAGAGAGGACCACTCCACAGACTACACACTCTCCGAAAGAGCCCTCCGTAAGCTTGC 3782
QY 90 Trr-----ProProAlaProGlu 95
Db 3781 TGGGGGGGGCGAGAGTCTGACTGCTGCTGAGAGAGTAATAGCCCTCCGCGCGCA 3722
QY 96 ValaAaPAppArgProGIn-----GluGlu 103
Db 3721 GAGAGCCGCGCGCCGACAGCTGCCACCGCCACCAAGATAGCCGCGCGCTGCG 3662
QY 104 ProAaPleuAaPProProArgGluGlu 112
Db 3661 CCGCACTGGAGGACCAACCAAGAGAG 3635

RESULT 10
US-08-458-240-1/c
; Sequence 1, Application US/08458240
; Patent No. 6143727
; GENERAL INFORMATION:
; APPLICANT: Roop, Dennis R.
; APPLICANT: Rothmigel, Joseph A.
; APPLICANT: Greenhalgh, David A.
; TITLE OF INVENTION: SPECIFIC EXPRESSION VECTORS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LYON & LYON
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,240
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,930
; FILING DATE:
; APPLICATION NUMBER: 07/876,286
; FILING DATE: April 30, 1992
; APPLICATION NUMBER: No. 6143727 yet assigned (204/132)
; FILING DATE: October 29, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weidburg, Richard J.
; REGISTRATION NUMBER: 32,327

```

REFERENCE/DOCKET NUMBER: 204/152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6530 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-458-240-1

Alignment Scores:
Pred. No.: 0.0028 Length: 6530
Score: 181.00 Matches: 50
Percent Similarity: 39.60% Conservative: 9
Best Local Similarity: 33.56% Mismatches: 46
Query Match: 26.16% Indels: 44
DB: 3 Gaps: 6

US-09-994-365-3 (1-114) x US-08-458-240-1 (1-6530)

QY 8 ProProAlaGluAspArgGluGluAlaGlySerProThrLeu-----21
DB 4081 CCACTTCCAGAGCCGCCACAGAGAGCGGCTCCGAGCTGAGCCACCGCTCCGCT 4022

QY 22 -----ProGlnGlyProProVal---ProGlyAspProTrpProGlyAla 35
DB 4021 CCGAGTAGCTCTCCGACACCGCCGCGCTCGCTCCGAGAGACCACTCCGACGCCA 3962

QY 36 ProProLeu---PheGluAspProProThrArgProSerArgProTrpArgAspLeu 54
DB 3961 CCGCGCTGCCCCCGGAAGAGCCCGCCACAGCCACCGCGCTCCGAGTAGCTTCCA 3902

QY 55 ProGluThrGlyValTrpProGluProProArgThrAspProProGlnProProArg 74
DB 3901 CCGAGACCAACCGCTGCTCCGACACCGCTGAGTAGAGCCACCGCGCCGCGCG 3842

QY 75 ProAspAspProTrpProAlaGlyProGlnProProGluAsnPro-----89
DB 3841 CCAAGAGAGCACTCCACAGCTACCACTCTCCGGAAGAGCCCTCCGTAGCTTGC 3782

QY 90 Trp-----ProProAlaProGlu 95
DB 3781 TGGGGGGCGCAGAGGCTGTGACTGCTGTGAGAGAGATATAGCCCCCTCCGCGCCA 3722

QY 96 ValAspAsnArgProGln-----GluGlu 103
DB 3721 GAGAGCCGCCCGCCGACACTGCCACCGCCAGCATATAGCCGCGCGCGCTGCCG 3662

QY 104 ProAspLeuAspProProArgGluGlu 112
DB 3661 CCGCAACTGAGAGCCACCAAGAGAG 3635

RESULT 11
PCT-US93-03993-1/c
Sequence 1, Application PC/TUS9303993
GENERAL INFORMATION:
APPLICANT: Roop, Dennis R.
APPLICANT: Rothnagel, Joseph A.
APPLICANT: Greenhalgh, David A.
TITLE OF INVENTION: CONSTITUTIVE AND INDUCIBLE EPIDERMAL
TITLE OF INVENTION: VECTOR SYSTEMS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03993
FILING DATE: 19930428
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5405
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
TELEX: 762829
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6530 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US93-03993-1

Alignment Scores:
Pred. No.: 0.0028 Length: 6530
Score: 181.00 Matches: 50
Percent Similarity: 39.60% Conservative: 9
Best Local Similarity: 33.56% Mismatches: 46
Query Match: 26.16% Indels: 44
DB: 5 Gaps: 6

US-09-994-365-3 (1-114) x PCT-US93-03993-1 (1-6530)

QY 8 ProProAlaGluAspArgGluGluAlaGlySerProThrLeu-----21
DB 4081 CCACTTCCAGAGCCGCCACAGAGAGCGGCTCCGAGCTGAGCCACCGCTCCGCT 4022

QY 22 -----ProGlnGlyProProVal---ProGlyAspProTrpProGlyAla 35
DB 4021 CCGAGTAGCTCTCCGACACCGCCGCTGCTCCGAGAGACCACTCCGACGCCA 3962

QY 36 ProProLeu---PheGluAspProProThrArgProSerArgProTrpArgAspLeu 54
DB 3961 CCGCGCTGCCCCCGGAAGAGCCCGCCACAGCCACCGCGCTCCGAGTAGCTTCCA 3902

QY 55 ProGluThrGlyValTrpProGluProProArgThrAspProProGlnProProArg 74
DB 3901 CCGAGACCAACCGCTGCTCCGACACCGCTGAGTAGAGCCACCGCGCCGCGCG 3842

QY 75 ProAspAspProTrpProAlaGlyProGlnProProGluAsnPro-----89
DB 3841 CCAAGAGAGCACTCCACAGCTACCACTCTCCGGAAGAGCCCTCCGTAGCTTGC 3782

QY 90 Trp-----ProProAlaProGlu 95
DB 3781 TGGGGGGCGCAGAGGCTGTGACTGCTGTGAGAGAGATATAGCCCCCTCCGCGCCA 3722

QY 96 ValAspAsnArgProGln-----GluGlu 103
DB 3721 GAGAGCCGCCCGCCGACACTGCCACCGCCAGCATATAGCCGCGCGCGCTGCCG 3662

QY 104 ProAspLeuAspProProArgGluGlu 112
DB 3661 CCGCAACTGAGAGCCACCAAGAGAG 3635

RESULT 12
US-09-894-844-103/c
Sequence 103, Application US/09894844

Patent No. 6686166
 GENERAL INFORMATION:
 APPLICANT: Behr, Marcel
 APPLICANT: Small, Peter
 APPLICANT: Scholnik, Gary
 APPLICANT: Wilson, Michael A.
 TITLE OF INVENTION: Molecular Differences Between Species of
 TITLE OF INVENTION: the M. Tuberculosis Complex
 FILE REFERENCE: STAN102CON
 CURRENT APPLICATION NUMBER: US/09/894,844
 CURRENT FILING DATE: 2001-06-27
 PRIOR APPLICATION NUMBER: 09/318,191
 PRIOR FILING DATE: 1999-05-25
 PRIOR APPLICATION NUMBER: 60/097,936
 PRIOR FILING DATE: 1998-08-25
 NUMBER OF SEQ ID NOS: 137
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 103
 LENGTH: 1854
 TYPE: DNA
 ORGANISM: Mycobacteria tuberculosis
 US-09-994-844-103

Alignment Scores:
 Pred. No.: 0.000843 Length: 1854
 Score: 180.50 Matches: 53
 Percent Similarity: 36.71% Conservative: 50
 Best Local Similarity: 33.54% Mismatches: 50
 Query Match: 26.08% Indels: 50
 Gaps: 7

US-09-994-365-3 (1-114) x US-09-894-844-103 (1-1854)

Qy 5 ProSerHisProProAlaGluAspArgGluAlaGlySerProThrLeuProGlnGly 24
 Db 1190 CCGCGGCGCCCGCGGTCGCTACACAGACCCCGGAGATCGCGCGCCACCAAGCA 1131
 Qy 25 Pro-----ProValProGlyAspProTrpProGlyAlaProPro 37
 Db 1130 CCGAGCGCGCGCTTACCAACCAACAGCGCGGAGATCGGTCGCGCGCGCGCGCG 1071
 Qy 38 LeuPheGluAspPro-----ProProThrArgProSerArgProTrpArgAspLeuPro 55
 Db 1070 TTACCATCAAGCCACAGCGCGCCGATCACCGCGCGCGCGCGCGCGCGCGCGCG 1017
 Qy 56 GluThrGlyValTrpPro--ProGluProProArgThrAsp-----CCG 68
 Db 1016 AAGCTTCGTGTGCGCGCGGTCCGCGTCCGCGAGCGCGTCCGCGCGCGCGCGCG 957
 Qy 69 -----ProProGlnProProArgProAspAsp 77
 Db 956 TTGCGCAACAACAAGCGCTGCTCCGCCGCTTGCGCGCTGACCGCGAAGCCGCCACC 897
 Qy 78 ProTrp-----ProAlaGlyPro-----83
 Db 896 CCTGTGACGAGTCCATCGGTGCGCGCGCCCAAGCCAGCCGACCGCGCGCGAG 837
 Qy 84 -----GlnProProGluAsnProTrpProProAlaProGluValAsp 97
 Db 836 CCGAAGGCAAGCGCGCTCGCGCGCGCGAGCAGCAGCGCGCGCGAGCGCGCGG 777
 Qy 98 AsnArgProGlnGluGluProAspLeuAsp--ProProArgGluGluTrpArg 114
 Db 776 AGATGCCCATCGAGGGCGGTGCTCGTGCACCGCGCGCGCGCGCGCGT 725

RESULT 13
 US-09-060-756-4/c
 Sequence 4, Application US/09060756
 Patent No. 6183957
 GENERAL INFORMATION:
 APPLICANT: Cole, Stewart
 APPLICANT: Buchrieser-Brosch, Roland
 APPLICANT: Gordon, Stephen

APPLICANT: Billault, Alain
 TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
 TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
 TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
 FILE REFERENCE: 3495-0169
 CURRENT APPLICATION NUMBER: US/09/060,756
 CURRENT FILING DATE: 1998-04-16
 NUMBER OF SEQ ID NOS: 743
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 4
 LENGTH: 1280
 TYPE: DNA
 ORGANISM: Mycobacterium tuberculosis
 US-09-060-756-4

Alignment Scores:
 Pred. No.: 0.000625 Length: 1280
 Score: 180.00 Matches: 49
 Percent Similarity: 44.00% Conservative: 6
 Best Local Similarity: 39.20% Mismatches: 53
 Query Match: 26.01% Indels: 17
 Gaps: 6

US-09-994-365-3 (1-114) x US-09-060-756-4 (1-1280)

Qy 5 ProSerHisProProAlaGluAspArgGluAlaGlySerProThrLeuProGlnGly 24
 Db 869 CCACCGCGCGCGCGGTGTCGCGCGCGCTTAAGCTCGCGCGCTTGAGCGCGCGCGCG 810
 Qy 25 -----ProProValProGlyAspProTrpProGlyAlaProProLeu 38
 Db 809 CCGTACCCCATTAAGTACGACCGCGTCCG-----CGTTCCACCGCGCGCGCGCTTA 756
 Qy 39 PheGluAspPro--ProProThrArgProSerArgProTrpArgAspLeuProGluThr 57
 Db 755 GCGTTACCGCGATTCGCGCGATGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 696
 Qy 58 GlyValTrpProProGluProProArgThr--AspProProGlnProProArgPro 75
 Db 695 CCG 636
 Qy 76 -----AspAspProTrp-----ProAlaGlyProGlnProProGluAsnProTrp 90
 Db 635 CTGACAACAAGACCGCGCGGTGCGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 576
 Qy 91 ProProAlaProGluValAspAsnArgProGlnGluProProAspLeuAspPro-ProAr 110
 Db 575 CCG 516
 Qy 110 GlnGluTrpArg 114
 Db 515 CCGTCCCAACCGG 503

RESULT 14
 US-09-670-314-4/c
 Sequence 4, Application US/09670314
 Patent No. 6492506
 GENERAL INFORMATION:
 APPLICANT: Cole, Stewart
 APPLICANT: Buchrieser-Brosch, Roland
 APPLICANT: Gordon, Stephen
 APPLICANT: Billault, Alain
 TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
 TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
 TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
 FILE REFERENCE: 3495-0169
 CURRENT APPLICATION NUMBER: US/09/670,314
 CURRENT FILING DATE: 2001-01-12
 PRIOR APPLICATION NUMBER: 09/060,756
 PRIOR FILING DATE: 1998-04-16
 NUMBER OF SEQ ID NOS: 743
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 4

LENGTH: 1280
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
US-09-670-314-4

Alignment Scores:

Score: 0.000625 Length: 1280
Percent Similarity: 180.00 Matches: 49
Best Local Similarity: 44.00% Conservative: 6
Query Match: 39.20% Mismatches: 53
DB: 26.01% Indels: 17
Gaps: 6

US-09-994-365-3 (1-114) x US-09-670-314-4 (1-1280)

Qy 5 ProserHisProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGly 24
Db 869 CCACCGCGCCCGCGGTGTCGCCGACGCTTAAGCTGCGCGCCCTTCGACGCGCGCGCG 810
Qy 25 -----ProProValProGlyAspProTrpProGlyAlaProProLeu 38
Db 809 CCGCTACCCCACTAAGTACCGCGGTGCG-----CGTTCCACCGCGCGCGCGCGTA 756
Qy 39 PheGluAspPro---ProProThrArgProSerArgProTrpArgAspLeuProGluThr 57
Db 755 GCGTTACCGCGGATTCGCGCGATGCGCGCGCGCGCGGACGACGCGCGCGCGCATG 696
Qy 58 GlyValTrpProProGluProGluProArgThr---AspProProGluProProArgPro--- 75
Db 695 CCG 636
Qy 76 -----AspAspProTrp-----ProAlaGlyProGlnProProGluAsnProTrp 90
Db 635 CTGACAAACAGACGCGCGCGGTGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 576
Qy 91 ProProAlaProGluValAspAsnArgProGlnGluProAspLeuAspPro-ProAr 110
Db 575 CCG 516
Qy 110 GGUgluTrpArg 114
Db 515 CCGTCCCGCGCGCG 503

RESULT 15

US-09-128-155-16
Sequence 16, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 152331
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(152331)
OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

Alignment Scores:

Pred. No.: 0.0852 Length: 152331
Score: 179.50 Matches: 45

Percent Similarity: 40.00% Conservative: 1
Best Local Similarity: 39.13% Mismatches: 16
Query Match: 25.94% Indels: 54
DB: 3 Gaps: 2

US-09-994-365-3 (1-114) x US-09-128-155-16 (1-152331)

Qy 8 ProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGlyProProVal 27
Db 21934 CCCCCCGCCCCCG 21993
Qy 28 ProGly---AspProTrpProGlyAlaProProLeuPheGluAspProProThrArg 46
Db 21994 CCG 22053
Qy 47 ProSerArgProTrpArgAspLeuProGluThrGlyValTrpProProGluProProArg 66
Db 22054 CCCCCACACCGCGCGCGCACGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22113
Qy 67 Thr-----AspProProGlnProProArg 74
Db 22114 AGCGGAGCG 22173
Qy 75 ProAspAspProTrpProAlaGlyProGlnProProGluAsnProTrpProProAlaPro 94
Db 22174 CCG 22231
Qy 95 GluValAspAsnArgProGlnGluProAspLeuAspProPro 109
Db 22232 AGCGCGACCG 22276

Search completed: January 12, 2005, 21:17:28
Job time : 6198 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_p2n model

Run on: January 12, 2005, 16:40:28 ; Search time 454 Seconds

(without alignments)
1442.800 Million cell updates/sec

Title: US-09-994-365-3

Perfect score: 692
Sequence: 1 SEGHPSHPAEDREAGSPT.....EVDNRQEPDLPPEEYR 114

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+g2n.model -DEV=xlh
-Q=/cg2_1/USPTO.epool.h/US0994365/runat_12012005.164014.11190/app.query.fasta.1.263
-DB=Published Applications NA -QFMT=fastap -SUFFIX=p2n.rmpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blonum62
-TRANS=human40.ccl -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=local -OUTPMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US0994365@cgn_1_1480@runat_12012005.164014.11190
-NCPU=6 -ICPU=3 -NO MMAP -LARGOUDERY -NEG SCORES=0 -WAIT -DSBLOCLCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOB=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:*

1:	/cg2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2:	/cg2_6/ptodata/1/pubpna/PTCT_NEM_PUB.seq:*
3:	/cg2_6/ptodata/1/pubpna/US06_NEM_PUB.seq:*
4:	/cg2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5:	/cg2_6/ptodata/1/pubpna/PTCTUS_PUBCOMB.seq:*
6:	/cg2_6/ptodata/1/pubpna/US07_NEM_PUB.seq:*
7:	/cg2_6/ptodata/1/pubpna/US08_NEM_PUB.seq:*
8:	/cg2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9:	/cg2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10:	/cg2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11:	/cg2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12:	/cg2_6/ptodata/1/pubpna/US09_NEM_PUB.seq:*
13:	/cg2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
14:	/cg2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
15:	/cg2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
16:	/cg2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
17:	/cg2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
18:	/cg2_6/ptodata/1/pubpna/US10_NEM_PUB.seq:*
19:	/cg2_6/ptodata/1/pubpna/US11_NEM_PUB.seq:*
20:	/cg2_6/ptodata/1/pubpna/US60_NEM_PUB.seq:*
21:	/cg2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

*

Result No.	Score	Query Match	Length	DB ID	Description
1	692	100.0	891	9	US-09-994-365-1
2	692	100.0	2997	9	US-09-994-365-10
3	692	100.0	3001	9	US-09-994-365-4
4	692	100.0	25235	15	US-10-164-230-2
5	692	100.0	55050	17	US-10-467-752-4
6	486	70.2	565	15	US-10-029-386-5700
7	441	63.7	367378	15	US-10-312-861-1
8	314	45.4	157	15	US-10-029-386-19510
9	199	28.8	711	16	US-10-282-122A-31860
10	198.5	28.7	2772	16	US-10-282-122A-28290
11	197	28.5	573	17	US-10-767-701-4301
12	196	28.3	766	18	US-10-425-115-82176
13	193	27.9	985	18	US-10-425-115-91623
14	190.5	27.5	446	9	US-09-864-761-20689
15	190	27.4	420	17	US-10-021-332-9375
16	189.5	27.4	815	16	US-10-424-599-20495
17	188.5	27.2	600	18	US-10-363-345A-39087
18	188.5	27.2	600	18	US-10-363-345A-39088
19	188	27.2	545	17	US-10-437-963-56258
20	188	27.2	1493	15	US-10-029-386-25133
21	187.5	27.1	916	18	US-10-425-115-47293
22	187.5	27.1	1327	16	US-10-398-221-1265
23	186.5	27.0	629	17	US-10-021-332-9375
24	186.5	26.9	925	17	US-10-437-963-44536
25	186	26.9	1455	16	US-10-282-122A-28683
26	186	26.9	12733	14	US-10-032-393-47
27	186	26.9	12739	14	US-10-032-393-8
28	185.5	26.8	588	17	US-10-021-332-9377
29	185.5	26.8	1245	17	US-10-437-963-94850
30	185.5	26.8	1744	17	US-10-437-963-19774
31	184.5	26.7	485	16	US-10-424-599-65670
32	183.5	26.5	3163	15	US-10-017-161-1857
33	183.5	26.5	3163	15	US-10-292-796-1513
34	183	26.4	590	18	US-10-425-115-133228
35	182.5	26.4	1083	15	US-10-029-386-20723
36	182	26.3	717	16	US-10-424-599-11376
37	182	26.3	821	18	US-10-425-115-131043
38	182	26.3	1848	16	US-10-282-122A-28602
39	182	26.3	114733	15	US-10-148-806-3
40	181.5	26.2	903	17	US-10-437-963-85740
41	181	26.2	674	16	US-10-424-599-69089
42	181	26.2	778	16	US-10-424-599-54839
43	181	26.2	791	16	US-10-424-599-64474
44	181	26.2	862	17	US-10-437-963-28390
45	180.5	26.1	497	16	US-10-424-599-133788

ALIGNMENTS

RESULT 1
US-09-994-365-1
Sequence 1, Application US/0994365
Patent No. US20020115148A1
GENERAL INFORMATION:
APPLICANT: Charmsley, Patrick
APPLICANT: Moss, Patrick
TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
FILE REFERENCE: CEC118109
CURRENT APPLICATION NUMBER: US/09/994,365
PRIOR FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: US 60/253,592
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/256,839
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 891
TYPE: DNA

ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (64)..(471)
 US-09-994-365-1

Alignment Scores:

Pred. No.:	1,54e-47	Length:	891
Score:	692.00	Matches:	114
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-994-365-3 (1-114) x US-09-994-365-1 (1-891)

QY 1 SerGIUGlYHISProSerHISProProAlaGluAspArgGluGluAlaGlySerProThr 20
 Db 130 AGCGAGGGCCACCCCTCTCAACCCGACAGAGACCGAGAGGAGGAGGCTCCCAACA 189
 QY 21 LeuProGlnGlyProProValProGlyAspProTyrProGlyAlaProProLeuPheGlu 40
 Db 190 TTGCTCAGGGCCCCCAGTCCCGGTGACCTTGCCAGGGGCAACCCCTCTCTTGA 249
 QY 41 AspProProProThrArgProSerArgProTyrArgAspLeuProGluThrGlyValTyr 60
 Db 250 GATCCTCCGCTACCCGCGCCAGTGTCTCTGAGAGACCTGCTGAACCTGAGCTGG 309
 QY 61 ProProGluProProAlaGlnThrArgProGlnProProAlaArgProAspProTyrPro 80
 Db 310 CCCCTGAACCGCTTGAACGAGATCTCTCAACCTCCGCGCTGACGACCTTGGCCG 369
 QY 81 AlaGlyProGlnProProGluAspProTyrProProAlaProGluValAspAsnArgPro 100
 Db 370 GCAGAGACCCAGCCCGCCAGAAACCCCTGGCTCTCTGAGGTGACACCGACT 429
 QY 101 GlnGluGluProAspLeuAspProProArgGluGluTyrArg 114
 Db 430 CAGAGAGCCAGACCTAGACCCCGGGAGAGATACAGA 471

RESULT 2

US-09-994-365-10
 ; Sequence 10, Application US/09994365
 ; Patent No. US20020115148A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Charmley, Patrick
 ; APPLICANT: Moss, Patrick
 ; APPLICANT: McEuen, Mark
 ; TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
 ; FILE REFERENCE: CECH18109
 ; CURRENT APPLICATION NUMBER: US/09/994,365
 ; PRIOR FILING DATE: 2001-11-26
 ; PRIOR APPLICATION NUMBER: US 60/253,592
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: US 60/256,839
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 2997
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-994-365-10

Alignment Scores:

Pred. No.:	3.81e-47	Length:	2997
Score:	692.00	Matches:	114
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-994-365-3 (1-114) x US-09-994-365-10 (1-2997)

QY 1 SerGIUGlYHISProSerHISProProAlaGluAspArgGluGluAlaGlySerProThr 20
 Db 2213 AGCGAGGGCCACCCCTCTCAACCCGACAGAGACCGAGAGGAGGAGGCTCCCAACA 2272
 QY 21 LeuProGlnGlyProProValProGlyAspProTyrProGlyAlaProProLeuPheGlu 40
 Db 2273 TTGCTCAGGGCCCCCAGTCCCGGTGACCTTGCCAGGGGCAACCCCTCTCTTGA 2332
 QY 41 AspProProProThrArgProSerArgProTyrArgAspLeuProGluThrGlyValTyr 60
 Db 2333 GATCCTCCGCTACCCGCGCCAGTGTCTCTGAGAGACCTGCTGAACCTGAGCTGG 2392
 QY 61 ProProGluProProAlaGlnThrArgProGlnProProAlaArgProAspProTyrPro 80
 Db 2393 CCCCTGAACCGCTTGAACGAGATCTCTCAACCTCCGCGCTGACGACCTTGGCCG 2452
 QY 81 AlaGlyProGlnProProGluAspProTyrProProAlaProGluValAspAsnArgPro 100
 Db 2453 GCAGAGACCCAGCCCGCCAGAAACCCCTGGCTCTCTGAGGTGACACCGACT 2512
 QY 101 GlnGluGluProAspLeuAspProProArgGluGluTyrArg 114
 Db 2513 CAGAGAGCCAGACCTAGACCCCGGGAGAGATACAGA 2554

RESULT 3

US-09-994-365-4
 ; Sequence 4, Application US/09994365
 ; Patent No. US20020115148A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Charmley, Patrick
 ; APPLICANT: Moss, Patrick
 ; APPLICANT: McEuen, Mark
 ; TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
 ; FILE REFERENCE: CECH18109
 ; CURRENT APPLICATION NUMBER: US/09/994,365
 ; PRIOR FILING DATE: 2001-11-26
 ; PRIOR APPLICATION NUMBER: US 60/253,592
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: US 60/256,839
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 3001
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-994-365-4

Alignment Scores:

Pred. No.:	3.81e-47	Length:	3001
Score:	692.00	Matches:	114
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-994-365-3 (1-114) x US-09-994-365-4 (1-3001)

QY 1 SerGIUGlYHISProSerHISProProAlaGluAspArgGluGluAlaGlySerProThr 20
 Db 2217 AGCGAGGGCCACCCCTCTCAACCCGACAGAGACCGAGAGGAGGAGGCTCCCAACA 2276
 QY 21 LeuProGlnGlyProProValProGlyAspProTyrProGlyAlaProProLeuPheGlu 40
 Db 2277 TTGCTCAGGGCCCCCAGTCCCGGTGACCTTGCCAGGGGCAACCCCTCTCTTGA 2336
 QY 41 AspProProProThrArgProSerArgProTyrArgAspLeuProGluThrGlyValTyr 60
 Db 2337 GATCCTCCGCTACCCGCGCCAGTGTCTCTGAGAGACCTGCTGAACCTGAGCTGG 2396
 QY 61 ProProGluProProAlaGlnThrArgProGlnProProAlaArgProAspProTyrPro 80

Db 2397 CCCCCGACCGCCTAGACGATCTCTCAACCTCCCGGCTGACGACCTTGCCG 2456
 Qy 81 AlaglyProgluProProgluAenProTrpProProAlaProgluValaAspAenArgPro 100
 Db 2457 GCGAGACCCCAAGCCCAAGAAACCCCTGCTCTGCTCCCTGAGGTGACACCACT 2516
 Qy 101 GlnGluGluProAspLeuAspProProArgGluGluArg 114
 Db 2517 CAGAGAGGACCAAGCCTAGACCCCAAGGAGAGATACAGA 2558

RESULT 4

US-10-164-230-2
 ; Sequence 2, Application US/10164230
 ; Publication No. US20030170652A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Inoko, Hidetoshi
 ; APPLICANT: Tamiya, Gen
 ; TITLE OF INVENTION: METHOD OF TESTING FOR PSORIASIS VULGARIS
 ; FILE REFERENCE: 06501-112US1
 ; CURRENT APPLICATION NUMBER: US/10/164,230
 ; PRIOR FILING DATE: 2002-09-04
 ; PRIOR APPLICATION NUMBER: PCT/JP00/08624
 ; PRIOR FILING DATE: 2000-12-06
 ; PRIOR APPLICATION NUMBER: JP 11/346867
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 25235

; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: (1)...(420)
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: (1282)...(1405)
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: (1602)...(1702)
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: (1602)...(1631)
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: (2352)...(2364)
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: (6287)...(6509)
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: (10417)...(10493)
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: (14244)...(14407)
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: (14244)...(14344)
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: (25190)...(25235)
 ; US-10-164-230-2

Alignment Scores:

Pred. No.: 1.86e-46 Length: 25235
 Score: 692.00 Matches: 114
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 15 Gaps: 0

US-09-994-365-3 (1-114) x US-10-164-230-2 (1-25235)

Qy 1 SerGluGluYHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThr 20
 Db 1766 AGCGAGGGCCACCCCTCTCAACCCGACGAGACCGAGAGAGGACGCTCCCAACA 1825
 Qy 21 LeuProGluGlyProProValProGlyAspProTrpProGlyValaProPoleuPheGlu 40
 Db 1826 TTGCTCAGGGGCCCCCAAGTCCCGGTGACCTTGGCCAGGGGCAACCCCTCTTTGAA 1885
 Qy 41 AspProProProThrArgProSerArgProTrpArgAspLeuProGluTrpGlyValTrp 60
 Db 1886 GATCTCCGCTCAACCCGACCTGCTGAGAGACCTGCTGAACTGAGATGTGG 1945
 Qy 61 ProProGluProProArgTrpAspProProGluProProArgProAspAspProTrpPro 80
 Db 1946 CCCCCTGAACCGCCTAGAACGATCTCTCAACCTCCCGGCTGACGACCTTGCCG 2005
 Qy 81 AlaglyProgluProProgluAenProTrpProProAlaProgluValaAspAenArgPro 100
 Db 2006 GCGAGACCCCAAGCCCAAGAAACCCCTGCTCTGCTCCCTGAGGTGACACCACT 2065
 Qy 101 GlnGluGluProAspLeuAspProProArgGluGluArg 114
 Db 2066 CAGAGAGGACCAAGCCTAGACCCCAAGGAGAGATACAGA 2107

RESULT 5

US-10-467-752-4
 ; Sequence 4, Application US/10467752
 ; Publication No. US20040161759A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lench, et al.
 ; TITLE OF INVENTION: Test and Model for Inflammatory disease
 ; FILE REFERENCE: 2003882-0009
 ; CURRENT APPLICATION NUMBER: US/10/467,752
 ; PRIOR FILING DATE: 2003-08-13
 ; PRIOR APPLICATION NUMBER: PCT/GB02/00653
 ; PRIOR FILING DATE: 2002-02-13
 ; PRIOR APPLICATION NUMBER: GB0103514.6
 ; NUMBER OF SEQ ID NOS: 109
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 55050

; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (13351)...(13351)
 ; OTHER INFORMATION: n is a or t or g or c
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (13401)...(13401)
 ; OTHER INFORMATION: n is a or t or g or c
 ; US-10-467-752-4

Alignment Scores:

Pred. No.: 3.32e-46 Length: 55050
 Score: 692.00 Matches: 114
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 17 Gaps: 0

US-09-994-365-3 (1-114) x US-10-467-752-4 (1-55050)

Qy 1 SerGluGluYHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThr 20
 Db 27111 AGCGAGGGCCACCCCTCTCAACCCGACGAGACCGAGAGAGGACGCTCCCAACA 27170
 Qy 21 LeuProGluGlyProProValProGlyAspProTrpProGlyValaProPoleuPheGlu 40
 Db 27171 TTGCTCAGGGGCCCCCAAGTCCCGGTGACCTTGGCCAGGGGCAACCCCTCTTTGAA 27230
 Qy 41 AspProProProThrArgProSerArgProTrpArgAspLeuProGluTrpGlyValTrp 60

```
Db 27231 GATCTCCGCTACCCGCCAGCTGCTCCCTGAGAGACCTGCTGAACCTGAGTCTGG 27290
Qy 61 ProProGluProProArgThraProProGluProProArgProProArgProProPro 80
Db 27291 CCCCCGAAACCGCTAGAACGATCTCTCACTCCCGGCTGACGACCTTGGCGG 27350
Qy 81 AlaGlyProGluProProGluAsnProProArgProProAlaProGluValAspAsnArgPro 100
Db 27351 GCAAGACCCCGACCCCGAGAAACCCCTGCTGCTGCTGAGTGGAGAACCACT 27410
Qy 101 GlnGluGluProAspLeuAspProProArgGluGluTyrArg 114
Db 27411 CAGAGAGACCGACCTAGAACCCCGGAGAGAGTACAGA 27452

RESULT 6
US-10-029-386-5700
; Sequence 5700, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 5700
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AB023060.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.82
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.82
; OTHER INFORMATION: SWISSPROT HIT: B513178.1, EVALU6 6.20e-01
; OTHER INFORMATION: EST HUMAN HIT: B513178.1, EVALU6 0.00e+00
; OTHER INFORMATION: NT HIT: g115304354, EVALU6 0.00e+00
; US-10-029-386-5700

Alignment Scores:
Pred. No.: 4.6e-31 Length: 565
Score: 486.00 Matches: 79
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 70.23% Indels: 0
Gaps: 0

US-09-994-365-3 (1-114) x US-10-029-386-5700 (1-565)
Qy 36 ProProLeuPheGluAspProProProThraProProSerArgProTyrArgAspLeuPro 55
Db 1 CCCCCTCTCTTGAAGATCTCTCCCTCAACCGGCTGCTGCTGAGAGACTGCTCT 60
Qy 56 GlnThrgLlyValTyrProProGluProProArgThraProProGluProProArgPro 75
Db 61 GAAACTGGAAGTGGCCCTGAAACCCCTGAAACGAGATCTCTCAACTCTCCCGGCT 120
Qy 76 AspAspProTyrProAlaGlyProGluProGluAsnProProTyrProProAlaProGlu 95
Db 121 GACGACCTTGGCGCGGAGAGACCCCGACCAAGAAACCCCTGCTGCTGCTGAG 180
Qy 96 ValAspAsnArgProGluGluGluProAspLeuAspProProArgGluGluTyrArg 114
Db 181 GTGAGACCAACGACCTCAGAGAGAGCCAGACCTAGACCCCGGAGAAAGTACAG 237

RESULT 7
US-10-312-841-1/c
; Sequence 1, Application US/10312841
```

```
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/1208/WO
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: (3294164)
; US-10-312-841-1

Alignment Scores:
Pred. No.: 1.36e-24 Length: 3673778
Score: 441.00 Matches: 69
Percent Similarity: 85.96% Conservative: 29
Best Local Similarity: 60.53% Mismatches: 16
Query Match: 63.73% Indels: 0
Gaps: 0

US-09-994-365-3 (1-114) x US-10-312-841-1 (1-3673778)
Qy 1 SerGluGlyHisProSerHisProProAlaGluAspArgGluGluValGlySerProThr 20
Db 1426038 AAGGAAACCAACCCCTCTCAACCCGACCAACCAACCAACCAACCAACCAACCA 1425979
Qy 21 LeuProGluGluProProValProGluAspProTyrProGluValAspProLeuPheGlu 40
Db 1425978 TTACCTCAAAACCCCAATCCCGATACCTTAACCAAAACACCCCTCTTTTAA 1425919
Qy 41 AspProProProThraProProSerArgProTyrArgAspLeuProGluThrgLlyValTyr 60
Db 1425918 AATCTCCGCGTACCCGCGCAATCGTCTTAATAAACTAACTAACTAACTAA 1425859
Qy 61 ProProGluProProArgThraProProGluProProArgProProArgAspProTyrPro 80
Db 1425858 CCCCCTAAACCGGCTAAACGATCTCTCAACCTCCCGACCTTAACGACCTTAACCG 1425799
Qy 81 AlaGlyProGluProProGluAsnProProTyrProProAlaProGluValAspAsnArgPro 100
Db 1425798 ACAAAACCCCAACCCCAAAACCCCTTAACCTCTTAACCTTAATAAACAACGACCT 1425739
Qy 101 GlnGluGluProAspLeuAspProProArgGluGluTyrArg 114
Db 1425738 CAATAAAACCAACCTTAACCAACCCGAAATAATACAA 1425697

RESULT 8
US-10-029-386-19510
; Sequence 19510, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
; FILE REFERENCE: AEOMICA-X-2
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 19510
; LENGTH: 157
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
```

```
/ OTHER INFORMATION: MAP TO AB023060.1
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.82
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.82
/ OTHER INFORMATION: EST_HUMAN HIT: BF902421.1, EVALUATE 3.00e-03
/ OTHER INFORMATION: NT_HIT: G115304354, EVALUATE 2.00e-83
/ OTHER INFORMATION: SWISSPROT HIT: P13889, EVALUATE 3.00e-01
US-10-029-386-19510

Alignment Scores:
Pred. No.: 1,34e-17 Length: 157
Score: 314.00 Matches: 51
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 45.38% Indels: 0
DB: 15 Gaps: 0

US-09-994-365-3 (1-114) x US-10-029-386-19510 (1-157)
Qy 64 ProProArghThraPProGlnProArghProAspPProTTPProAlaGlyPro 83
Db 2 CCGCTTGAACGGATCTCTCTCAACCTCCGCGCTGACGACCTTGCGCGACGACCC 61
Qy 84 GlnProGluAsnProTTPProProAlaProGluValAspAsnArgProGlnGlu 103
Db 62 CAGCCCCAGAAAACCCCTGGCCCTCTGCCCTGAGGTGGACACGACCTCAGAGAG 121
Qy 104 ProAspLeuAspProProAlaGluGluTyrArg 114
Db 122 CCAGACTAGACCAACCCCGGAGAGTACAGA 154

RESULT 9
US-10-282-122A-31860/C
/ Sequence 31860, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Karl
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
```

```
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 31860
/ LENGTH: 711
/ TYPE: DNA
/ ORGANISM: Pseudomonas putida
US-10-282-122A-31860

Alignment Scores:
Pred. No.: 7.86e-08 Length: 711
Score: 199.00 Matches: 46
Percent Similarity: 44.95% Conservative: 3
Best Local Similarity: 42.20% Mismatches: 42
Query Match: 28.76% Indels: 18
DB: 16 Gaps: 6

US-09-994-365-3 (1-114) x US-10-282-122A-31860 (1-711)
Qy 5 ProSerHisProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGly 24
Db 446 CCGGATAGCGCACACCG-----TCACCGCGCTGCGG---TGG 411
Qy 25 ProProValPro---GlyAspProTTPProGlyAlaProBouleuPheGluAspProPro 43
Db 410 CCACACTTCGCGCTCCGACCATGAGCCACCGCGCCACACTT-----CCACACCA 357
Qy 44 ProThrArgProSerArgProTTPArgAspLeuProGluThrGlyValTTPProProGlu 63
Db 356 CCGTGGCCACACACCGCGCTTCCACACACCG-----TGGCACCGCCA 309
Qy 64 ProProArghThraP-----ProProGlnProProArghProAspPProTTPPro 80
Db 308 CCGCGCTTCCACACACCGCTGACACCGCCACCGCGCTTCCACCGCCACCGTGGCCA 249
Qy 81 AlaGlyProGlnProProGluAsnProTTPProProAlaProGluValAspAsnArgPro 100
Db 248 CCGCGCGCGCGCTTCCACCGCCACCGTGGCCACCGCGCGCCGACCTTCCACCGCCACCG 189
Qy 101 GlnGluGluProAspLeuAspProPro 109
Db 188 TGGCCACCGGCCACCGCCACCGCCACCG 162

RESULT 10
US-10-282-122A-28290/C
/ Sequence 28290, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Karl
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
```

RESULT 11
US-10-767-701-4301
; Sequence 4301, Application US/10767701
; Publication No. US20040112684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

```

QY      1 Ser1GluGln1sPProSerHisProProAlaGluAar-----ArgGluGln 15
      14 ACCCGGAGGCCAACCACACCCCCCCCCCGCGCGCGCCGACCAAGCGCGCGCGCGCGCGCGCG 73
QY      16 AlaGlySerProThrLeuProGlnGlyProProValProGlyAaSProTTrPro----- 33
      74 GCGCGCCCCCCCCCCCCCCCCCGCGCGCGCTCGCGCTCCCGGGGCGCGCGCGCGCGCGCGCG 133
QY      34 -----GlyAla-----ProPLeuPheGlnAaSProPro 43
      134 CCAAGTCCCCCGGAGCAGCGCGGTGCGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 184
QY      44 ProThrArgProSerArgProTTrArgAspLeuProGluThrGlyValTTrProProGlu 63
      185 CCCCCGATGCGCGCGCGCCCCCGGAGCGCAAGCCCCCCCCCTCGCG-----CCCGCGAAT 235
QY      64 ProProAlaGlnThrAaSProProGlnProProAlaArgProAaAaSProTTr-----Pro 80
      236 CCGCGTCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 295
QY      81 AlaGlyPro-GlnProProGluAaSProTTrProProAlaProGluValAaSPaAaArg-- 99
      296 GGGGGCGCGGAGTCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 355
QY      100 -----ProGlnGluGlnProAaSPaSPaSPaSPaSPaSPaSPaSPaSPaSPaSPaSPa 112
      356 CCCCCCGGAGCGACCGCGCGCGCGCGCGCGCGCGCGAGACCGCGCGCGCGCGCGCGCGCG 415
Db      112 uTyArg 114
      416 CCGCGGT 422

RESULT 12
US-10-425-115-82176
/ Sequence 82176, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 82176
/ LENGTH: 766

```



```

: TYPE: DNA
: ORGANISM: Zea mays
: FEATURE:
: OTHER INFORMATION: Clone ID: MRT4577_17495C.1
US-10-425-115-82176

Alignment Scores:
Pred. No.: 1,45e-07 Length: 766
Score: 196.00 Matches: 44
Percent Similarity: 41.51% Conservative: 0
Best Local Similarity: 41.51% Mismatches: 54
Query Match: 28,32# Indels: 8
DB: 18 Gaps: 2

US-09-994-365-3 (1-114) x US-10-425-115-82176 (1-766)

Qy 4 HisProSerHisProProAlaGluAspArgGluAlaGlySerProThrLeuProGln 23
Db 165 CACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCTCCTCACCACCCCCCCCCCCC
Qy 24 GlyProProValProGlyAspProTrpProGlyAlaProProLeuPheGluAspProPro 43
Db 225 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Qy 44 ProThrArgProSerArgProTrpTrpArgAspLeuProGluThrGlyAlaTrpProProGlu 63
Db 285 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Qy 64 ProProArgThrAspProProGlnProProArgProAspAspProTrpProAlaGlyPro 83
Db 330 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCTCACCACCCCCCCCCCCCCCCC
Qy 84 GlnProProGluAsnProTrpTrpProProAlaProGluValAspAsnArgProGlnGluGln 103
Db 390 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Qy 104 ProAspLeuAspProPro 109
Db 441 CCCCCCTCCCCCCCCCCC 458

RESULT 13
US-10-425-115-91623/c
: Sequence 91623, Application US/10425115
: Publication No. US20040214272A1
: GENERAL INFORMATION:
: APPLICANT: La Rosa, Thomas J.
: APPLICANT: Kovalic, David K.
: APPLICANT: Zhou, Yihua
: APPLICANT: Cao, Yongwei
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
: TITLE OF INVENTION: Plants
: FILE REFERENCE: 38-21(5322)B
: CURRENT APPLICATION NUMBER: US/10/425,115
: CURRENT FILING DATE: 2003-04-28
: NUMBER OF SEQ ID NOS: 369326
: SEQ ID NO 91623
: LENGTH: 985
: TYPE: DNA
: ORGANISM: Zea mays
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (1)..(985)
: OTHER INFORMATION: unsure at all n locations
: FEATURE:
: OTHER INFORMATION: Clone ID: MRT4577_183557C.1
US-10-425-115-91623

Alignment Scores:
Pred. No.: 3,06e-07 Length: 985
Score: 193.00 Matches: 45
Percent Similarity: 42.99% Conservative: 1
Best Local Similarity: 42.06% Mismatches: 51
Query Match: 27,89# Indels: 10

```

```

DB: 18 Gaps: 3
US-09-994-365-3 (1-114) x US-10-425-115-91623 (1-985)
Qy 5 ProSerHisProProAlaGluAspArgGluGluAlaGlySerProThrIleuProGlnGly 24
Db 864 CCCCCCAACCCCCCCCCCCCCCCCCCCCC-----TCCCCCCCCCCCCCCCCCCC 817
Qy 25 ProProValProGlyAspProTrpProGlyAlaProProIleuGluAspProProPro 44
Db 816 CCCCCCCCCCCCCCCCCCCCCCCCCCTTCCCAACCCCAACCCCAACCCCAACCC 757
Qy 45 ThrArgProSerArgProTrpArgAspIleuProGluThrGlyValTrpProGluPro 64
Db 756 CCCCCCCCCCCCCCCCC-----CCCCCCCCCCCCCCCCCCCCCCCCCCCC 709
Qy 65 ProArg-----ThrAspProProGlnProProArgProAspAspProTrpProAlaGly 82
Db 708 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCGAACCAACCCCCCCCC 649
Qy 83 ProGlnProProGluAsnProTrpProProAlaProGluValAspAsnArgProGlnGlu 102
Db 648 CCCCCCCCCCCCCCCCCCCCCCGACCAACCCCAACCCCAACCCCAACCCCAACCC 589
Qy 103 GluProAspIleuAspProPro 109
Db 588 CCCCCCCCCACCCCTCC 568

RESULT 14
US-09-864-761-20699/c
Sequence 20699, Application US/09864761
Patent No. US2002048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME- DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687

```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 11, 2005, 11:40:34 ; Search time 2364.82 Seconds
(without alignments)
1756.640 Million cell updates/sec

Title: US-09-994-365-3
Perfect score: 692
Sequence: 1 SEGHPSPAPADEREAGSPF.....EVDNRPEPDPDPPEEYR 114

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame_p2n.model -DEV=x1h
-Q=cg2_1/USPTO.epool.h/US0994365/runat_10012005_172232.6834/app.query.fasta_1.590
-DB=EST -QFMT=faa1ap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=prc -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0994365 @CCN 1.1 4385 @runat_10012005_172232.6834 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WANN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	559	80.8	634	7	CF764947 CES003088
2	551	79.6	593	7	CF765720 CES001471
3	541	78.2	383	2	AW315342 12593 MAR
4	507	73.3	416	9	CG481452 OST13885
5	506	73.1	422	1	AT596929 vj46e11.y
6	506	73.1	451	9	CG484009 OST17807
7	506	73.1	669	9	CG484609 OST18617
8	501	72.4	442	9	CG487403 OST22893
9	498	72.0	562	1	AA530301 vj46e11.x

10	471.5	68.1	475	9	CG473878	CG473878 OST1668 M
11	460	66.5	322	9	CG474695	CG474695 OST2738 M
12	446.5	64.5	332	1	AA763309	AA763309 vv989h03.x
13	441	63.7	386	9	CG474680	CG474680 OST2720 M
14	425	61.4	451	1	AA798896	AA798896 vv94e08.x
15	375	54.2	395	9	CG528207	CG528207 OST107284
16	363	52.5	283	9	CG474588	CG474588 OST2599 M
17	345	49.9	243	8	AQ357151	AQ357151 CITBI-B1-
18	298	43.1	204	1	AA733661	AA733661 vv74f01.x
19	283	40.9	379	1	AA791103	AA791103 vv91a02.x
20	233	33.7	489	8	BH098389	BH098389 RPCT-24-3
21	209	30.2	984	4	BG441224	BG441224 GA_Ea001
22	209	30.2	1380	9	CL058490	CL058490 CH216-88C
23	206	29.8	361	1	AA168568	AA168568 ms31c08.r
24	205.5	29.7	812	1	AG133085	AG133085 Pan trogl
25	205	29.6	1272	9	AG356574	AG356574 Mus muscu
26	205	29.6	1283	9	AG435406	AG435406 Mus muscu
27	204.5	29.6	1585	8	CC294035	CC294035 CH261-82A
28	203.5	29.4	977	9	CL488066	CL488066 SAIL_503
29	203	29.3	848	9	CNS02YYE	AL220271 Tetradon
30	202.5	29.3	1218	9	AG435362	AG435362 Mus muscu
31	202	29.2	1142	9	CL501710	CL501710 SAIL_702
32	201.5	29.1	837	4	BG530104	BG530104 602558771
33	201	29.0	1051	9	CL119109	CL119109 ISB1-75M6
34	201	29.0	2131	8	CC296269	CC296269 CH261-104
35	200.5	29.0	1094	9	CC908599	CC908599 t043p13ba
36	200.5	29.0	1446	9	CL082756	CL082756 CH216-170
37	200	28.9	1648	9	AG390465	AG390465 Mus muscu
38	200	28.9	1691	9	AG341104	AG341104 Mus muscu
39	199.5	28.8	527	9	BX200083	BX200083 Bv19125
40	199.5	28.8	609	6	BY719125	BY719125 Pan trogl
41	199.5	28.8	663	9	AG132227	AG132227 SAIL_534
42	199.5	28.8	1331	9	CL490238	CL490238 SAIL_534
43	199	28.8	664	9	BX247035	BX247035 Dario rer
44	199	28.8	964	4	BM416247	BM416247 OP2135 M
45	199	28.8	1038	9	CL478560	CL478560 SAIL_292

ALIGNMENTS

RESULT 1
CF764947
LOCUS
DEFINITION
CF764947 Bos taurus skin cDNA library Bos taurus cDNA clone
634 bp mRNA linear EST 17-OCT-2003
CCL003088 5', mRNA sequence.

ACCESSION
CF764947
VERSION
CF764947.1 GI:37714166
KEYWORDS
EST.
SOURCE
Bos taurus (cow)
ORGANISM
Bos taurus

REFERENCE
Wang, Y.H., McWilliam, S. and Lehnert, S.
Transcription profiling of cattle skin
Unpublished (2003)
JOURNAL
COMMENT
Contact: Dr Yonhong Wang
Functional Genomics Lab
CSIRO Livestock Industries
Level 5, Queensland Biosciences Precinct, University of Queensland,
306 Carnody Road St. Lucia QLD Australia
Tel: 07 3214 2445
Fax: 07 3214 2685
Email: Yonhong.Wang@csiro.au
Plate: 40 row: G column: 07.
Location/Qualifiers
1..634
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Hereford Shorthorn"
/db_xref="taxon:9913"
/clone="CCL003088"

FEATURES
source

```

/sex="female"
/tissue_type="pooled"
/dev stage="Adult"
/lab_host="XLI-BlueMRF/strain"
/clone_1lb="Bos taurus skin cDNA library"
/notes="Organ: skin; Vector: Uni-ZAPXR; Site 1: EcorI;
Site 2: Xho I; Library made from pooled skin of adult
female Hereford-Shorthorn."

```

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 7.76e-25	634	92	5	17	0	0
Percent Similarity: 85.09%						
Best Local Similarity: 80.70%						
Query Match: 80.78%						

US-09-994-365-3 (1-114) x CF764947 (1-634)

```

Qy 1 SerGluglHisProSerHisProProAlaGluAspArgGluAlaGlySerProThr 20
Db 76 AGTGAAGACGAGCCCTCCCTCATCCAGAGAGATCTCAGAGAGAGGCGCTCCACCA 135
Qy 21 LeuProGluGlyProProValProGlyAspProTrpProGlyAlaProProLeuPheGlu 40
Db 136 TTGCCTCAGAGGCGCCCGCAATCCCTGATGACCCCTGGCCAGGCGCACCCCGCTTTGAG 195
Qy 41 AspProProProTrpArgProSerArgProTrpArgAspLeuProGluThrGlyValTyr 60
Db 196 GATCCTCAGAGGCGCCCGCAATCCCTGATGACCCCTGGCCAGGCGCACCCCGCTTTGAG 255
Qy 61 ProProGluProProArgTrpArgProProGluProProArgProProAspAspProTrp 80
Db 256 CCTCTGAACCCCTTAAGACTGATCCCTCACTCTGCGCTGACGACCCCTGAGCC 315
Qy 81 AlaGlyProGluProProGluAsnProTrpProProAlaProGluValAspAsnArgPro 100
Db 316 GCAAGAGCCGAGCCTCCAGAAACCCCTGGCCACCTGCGCTGAGCGACCAAGATCT 375
Qy 101 GlnGluGluProAlaPheAspProProArgGluGluTyrArg 114
Db 376 CACGAGAGCCAGACTTGACCCACCGAGGAGGAGTACAGA 417

```

RESULT 2

CF765720 593 bp mRNA linear EST 17-OCT-2003
LOCUS CF765720 CDS001471 Bos taurus skin cDNA library Bos taurus cDNA clone

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 593)
Wang, Y.H., McWilliam, S. and Lehnert, S.
Transcription profiling of cattle skin
Unpublished (2003)
Contact: Dr Yonghong Wang
Functional Genomics Lab
CSIRO Livestock Industries
Level 5, Queensland Biosciences Precinct, University of Queensland,
306 Carmody Road St. Lucia QLD Australia
Tel: 07 3214 2445
Fax: 07 3214 2685
Email: Yonghong.Wang@csiro.au
Plate: 25 row: B column: 04.
Location/Qualifiers
1. .593
/organism="Bos taurus"

```

/mol type="mRNA"
/strain="Hereford Shorthorn"
/db_xref="taxon:9913"
/clone="CCL001471"
/sex="female"
/tissue_type="pooled"
/dev stage="Adult"
/lab_host="XLI-BlueMRF/strain"
/clone_1lb="Bos taurus skin cDNA library"
/notes="Organ: skin; Vector: Uni-ZAPXR; Site 1: EcorI;
Site 2: Xho I; Library made from pooled skin of adult
female Hereford-Shorthorn."

```

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 2.21e-24	593	90	5	15	0	0
Percent Similarity: 86.36%						
Best Local Similarity: 81.82%						
Query Match: 79.62%						

US-09-994-365-3 (1-114) x CF765720 (1-593)

```

Qy 5 ProSerHisProProAlaGluAspArgGluAlaGlySerProThrLeuProGluGly 24
Db 88 CTTTCCCGCCATCCAGAGAGATCTCAGAGAGAGGCGCTCCACCATTTGCTCAGGCG 147
Qy 25 ProProValProGlyAspProTrpProGlyAlaProProLeuPheGluAspProPro 44
Db 148 CCCCAGATCCCTGATGACCCCTGCGCCAGGCGCACCCCGCTTTGAGGATCTCCACCT 207
Qy 45 ThrArgTrpProProTrpArgAspLeuProGluValTyrProProGluPro 64
Db 208 CCAAGCCCAATGCTCCGAGAGACTGCTGATTTGAGACTGAGCTCTGAAACC 267
Qy 65 ProArgTrpAspProProGluProProArgProAspAspProTrpProAlaGlyProGlu 84
Db 268 CTTAAGAGATGATCCCTCACTCTGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 327
Qy 85 ProProGluAsnProTrpProProAlaProGluValAspAsnArgProGluGluPro 104
Db 328 CTTCCAGAAACCCCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 387
Qy 105 AspLeuAspProProArgGluGluTyrArg 114
Db 388 GACCTTGACCCAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417

```

RESULT 3

AM315342 383 bp mRNA linear EST 09-JUL-2000
LOCUS AM315342 12593 MRC 2PTG Sus scrofa cDNA 5', mRNA sequence.

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

1 (bases 1 to 383)
Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J.,
Vallet, J., Wise, T., Rohrer, G.A., Perrea, G., Sultana, R.,
Quackenbush, J. and Keefe, J.W.
Porcine gene discovery by normalized cDNA-library sequencing and
EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smtth@mail.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCAGACG
Plate: 8 row: A column: 14
Seq primer: ATTAGGTGACATATAG.

FEATURES
Source Location/Qualifiers

1..383
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_id="MARC 2P1G"
/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

ORIGIN

Alignment Scores:
Pred. No.: 5,72e-24 Length: 383
Score: 541.00 Matches: 87
Percent Similarity: 86.24% Conservative: 7
Best Local Similarity: 79.82% Mismatches: 15
Query Match: 78.18% Indels: 0
DB: Gaps: 0

US-09-994-365-3 (1-114) x AW315342 (1-383)
Qy 1 SerGluGluHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThr 20
Db 57 AGCGAGAGACCAACCATCTCCGCCATCCACGAGGCGCTCAGAGAGAGGGCTCCCAACA 116
Qy 21 LeuProGluGlyProProValProGlyAspProTyrProGlyAlaProProLeuPheGlu 40
Db 117 TTGGCTGGGGCCCCCAATCCCGGTGACCTTGCGCAGGGGTAACCTCTATCTTTGAG 176
Qy 41 AspProProProThrArgProSerArgProTyrArgAspLeuProGluThrGlyValTyr 60
Db 177 GACCTCTCAGCTCCAGGCGCCAAATCGTCCCTCGAGAGACCTCGCATCTGAGTCTGG 236
Qy 61 ProProGluProProArgThrAspProGluProAlaProProArgProAspAspProTyr 80
Db 237 CCTCTTAACCCCTTAAGTATGATCTCCCTCAACCTCCCGCTGACGACCTCTGAGCA 296
Qy 81 AlaGlyProGluProProGluAspProTyrProProAlaProGluValAspAsnArgPro 100
Db 297 GCAGGAGCCCAAGCTCCAGAAACCCCTGCGCACTGCGCTGAGTGGACCAAGATCC 356
Qy 101 GlnGluGluProAspLeuAspProPro 109
Db 357 CGAGAGAGCCAGACCTTGACCCACC 383

RESULT 4
LOCUS CG481452 416 bp DNA linear GSS 01-OCT-2003
DEFINITION OST13885 Mus musculus 129Sv/Ev Mus musculus genomic clone, OST13885,
genomic survey sequence.
ACCESSION CG481452
VERSION CG481452.1 GI:37233834
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandeRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaling,C.,
Key,B.W., Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,

TITLE Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparke,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu Q., Person,C. and Sands,A.T.
JOURNAL Wnt1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
COMMENT Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
Omnibank

Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES
Source Location/Qualifiers

1..416
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST13885"
/cell_type="embryonic stem cell"
/clone_id="Mus musculus 129Sv/Ev"

ORIGIN

Alignment Scores:
Pred. No.: 7,16e-22 Length: 416
Score: 507.00 Matches: 80
Percent Similarity: 82.14% Conservative: 12
Best Local Similarity: 71.43% Mismatches: 20
Query Match: 73.27% Indels: 0
DB: Gaps: 0

US-09-994-365-3 (1-114) x CG481452 (1-416)
Qy 3 GlyHisProSerHisProProAlaGluAspArgGluGluAlaGlySerProThrLeuPro 22
Db 14 GGGACCCCTTCCGCGATCTACAGACACCAAGAGAGAGAGCTCCCAACATTCCT 73
Qy 23 GlnGlyProProValProGlyAspProTyrProGlyAlaProProLeuPheGluAspPro 42
Db 74 CTGGAGACCCCAATCCCTGTGATCTCCCTGGCGCGCTCTTGTGTGATGAACCT 133
Qy 43 ProProThrArgProSerArgProTyrArgAspLeuProGluThrGlyValTyrProPro 62
Db 134 CCGCTCTCAGGCTCCACCGTCCCTGAGAGATCTTCTGACAGTGGTGGCTGCCCCCA 193
Qy 63 GluProProArgThrAspProProGluProProArgProAspAspProTyrProAlaGly 82
Db 194 AAGCCCCCAAGCACTGATCCCTTAACCTCTCTGCTATGACCTGCGCAAGAGGA 253
Qy 83 ProGluProProGluAspProTyrProProAlaProGluValAspAsnArgProGlnGlu 102
Db 254 ACCGAGCCCCCAGAAACCCCTGGCTCTGCGCTGAGATGAGCATGATCTCAGGAG 313
Qy 103 GluProAspLeuAspProProArgGluGluTyrArg 114
Db 314 GAGCCAGACCTTGACCCACCCAGAAAGATATAGA 349

RESULT 5
LOCUS A1596929 422 bp mRNA linear EST 21-APR-1999
DEFINITION v146e11.y1 Stragagene mouse skin (#937313) Mus musculus cDNA clone
IMAGE:932108 5', mRNA sequence.
ACCESSION A1596929
VERSION A1596929.1 GI:4605977
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 422)
Marra,M., Hallier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,T.,

100

RESULT 7
CG484609
LOCUS
DEFINITION OS118617 Mus musculus 129Sv/Ev Mus musculus genomic clone OS118617,
 genomic survey sequence.
ACCESSION CG484609
VERSION CG484609.1 GI:37240590
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 669)
REFERENCE Zambrowicz, B. P., Abuhin, A., Ramirez-Solis, R., Richter, L. T.,
 Piotti, J., BeltrandelRio, H., Buxton, E. C., Edwards, J., Finch, R. A.,
 Fridele, C. J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jiaing, C.,
 Key, B. W., Jr., Klipp, P., Kohlhaufl, B., Ma, Z.-Q., Markesich, D.,
 Payne, R., Potter, D. G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
 Sparks, M. J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
 Zhu, Q., Person, C. and Sande, A. T.
 Wnt1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
JOURNAL Contact: Zambrowicz BP
 OmniBank
COMMENT Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: material@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap.
FEATURES Location/Qualifiers
source 1..669
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OS118617"
 /cell_type="embryonic stem cell"
 /clone_11b="Mus musculus 129Sv/Ev"
ORIGIN
 Alignment Scores:
 Pred. No.: 1,34e-21 Length: 669
 Score: 506.00 Matches: 80
 Percent Similarity: 82.14% Conservative: 12
 Best Local Similarity: 71.43% Mismatch: 20
 Query Match: 73.12% Indels: 0
 DB: 9 Gaps: 0
 US-09-994-365-3 (1-114) x CG484609 (1-669)
 Oy 3 G1yHispRoserHisPProProAlaGluuAspArgGluGluAlaGlySerProThrLeuPro 22
 ||||| ||||| ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 8 GGGCAGCCTTCTCCCGGATCTCAACAACAACCCAGAAAGAGAGAGATCCCGACCATGGCT 67
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 23 G1ng1yPProProAlProGlyAspProTrpProG1yAlaProProLeuPhGluAspPro 42
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 68 CTGGAGACCCCAATCCCTGGTGAATCCCTGGGCGGCGCTCTCTTGTGTGATGAACCT 127
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 43 ProProThraArgProSerArgProTrpArgAspLeuProGluThnGlyValTrpProPro 62
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 128 CGGCTCCAGGCTCCACCGTCCTCGGAGAGATCTCTGACAGTGTGCTGGGCGGCCCA 187
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 63 GluProProArgThraSpProGluInProProAlaPProAspAspProTrpProAlaGly 82
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 188 AAGCCCCCAAGACGATGCCCTTAACCTCCTGCTGATGAGACCTGGCGCAGCAGA 247
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Oy 83 ProGluInProProGluAsnProTrpProProAlaProGluValAspAsnArgProGluInu 102
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db	1248	ACCCAGCCCCAGAAAACCCCTGCGCTCTCTGCTCCCTGAGATGACACATGATCTCAGAG	307
Qy	103	GlupProaPleuAaspProProArgGlugluInuYrArg	114
Db	308	GAGCCAGACTTGAGACCCACCCAGAGAGATAGAGA	343
RESULT 8			
LOCUS	CG487403		
DEFINITION	CG487403 Mus musculus 129Sv/Ev Mus musculus genomic clone OST2893.		
ACCESSION	CG487403		
VERSION	CG487403.1		
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathia; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 442)		
TITLE	Zambrowicz, B. P., Abidin, A., Ramirez-Solis, R., Richter, L. J., Piggott, J., Beltrande-Rio, H., Buxton, E. C., Edwards, J., Finch, R. A., Fridele, C. J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B. W., Jr., Klipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Porter, D. G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M. J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C., and Sands, A. T.		
JOURNAL	Mnl kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention		
COMMENT	Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003) Contact: Zambrowicz BP OmniBank Lexicon Genetics Incorporated 4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: materials@lexgen.com Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11) Class: Gene trap. Location/Qualifiers		
FEATURES	source		
	1..442		
	/organism="Mus musculus"		
	/mol_type="genomic DNA"		
	/strain="129Sv/Ev"		
	/db_xref="taxon:10090"		
	/clone="OST2893"		
	/cell_type="embryonic stem cell"		
	/clone_lib="Mus musculus 129Sv/Ev"		
ALIGNMENT			
Pred. No.:	1.76e-21	Length:	442
Score:	501.00	Matches:	79
Percent Similarity:	82.73%	Conservative:	12
Best Local Similarity:	71.82%	Mismatches:	19
Query Match:	72.40%	Indels:	0
DB:	9	Gaps:	0
US-09-994-365-3 (1-114) x CG487403 (1-442)			
Qy	5	ProserHisPProProAlaGluAaspArgGluGluAlaGlySerProThrleuProGlnGly	24
Db	4	CCCTCTCCCGATCTACAGACACCCACAGAAAGAGAGACTCCACCACTTGCTCTGGGA	63
Qy	25	ProProValProGlyAaspProTrpProGlyValAlaProProleuPheGluAaspProPro	44
Db	64	CCCCCAATCCCTGTGATCCCTGCGCTGGGGCGGCTCTTTTGTGATGAACCTCCGCT	123
Qy	45	ThirArgProSerArgProTrpArgAaspLeuProGluThrGlyValTrpProGluPro	64
Db	124	COAGGCTCAACCGTCCCTGGAGAGATCTTCTGACAGTGGTGCCTGCCCCCAAGCCC	183
Qy	65	ProArgThrAaspProProGlnProProArgProAaspProTrpProAlaGlyProGln	84

```

Db      184 CCAGACGATGATCCCTTAAACCTCTCTGCGTATGACCCCTGGCAGACAGAAACCCAG 243
Qy      85  ProProGluAsnProTyrProProAlaProGluValAspAsnArgProGlnGluPro 104
Db      244  CCCCAGAAACCCCTGGCTCTCTGCGTATGAGACCATGAATCTCAGAGAGACCA 303
Qy      105  AspleAspProProArgGluGluTyrArg 114
Db      304  GACCTTGACCCACCCACGAGAAAGATATGA 333

RESULT 9
AA530301 562 bp mRNA linear EST 22-JUL-1997
LOCUS vJ46ell.r1 Strataegene mouse skin (#937313) Mus musculus cDNA clone
DEFINITION IMAGE:932108 5', mRNA sequence.
ACCESSION AA530301
VERSION AA530301.1 GI:2273007
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 562)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisell,S., Kucaba,T., Lacy,M., Le,M., Martin,U., Morris,M.,
Scheiblenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence scop: 221.
Location/Qualifiers
1..562
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:932108"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Strataegene mouse skin (#937313)"
/notes="Organ: skin; Vector: pBluescript SK-; Site 1:
Scor1; Site 2: Xho1; Cloned unidirectionally. Primer:
Oligo dt. Whole skin from 11 week old C57BL/6 female mice
Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
adaptor sequence: 5' GAATTCGACACGAG 3' ~3' adaptor
sequence: 5' CTCGAGTTTATTTTATTTT 3'"

ORIGIN
Alignment Scores:
Pred. No.: 3,42e-21 Length: 562
Score: 498.00 Matches: 79
Percent Similarity: 81.25% Conservative: 12
Best Local Similarity: 70.54% Mismatches: 21
Query Match: 71.97% Indels: 0
Gaps: 1 0

US-09-994-365-3 (1-114) x AA530301 (1-562)
GlyHisProSerHisProProAlaGluAspArgGluGluGlySerProThrLeuPro 22

```

Db	40	GGCAGCCTTTCTCCCGGATCTACAGACACCCAGAAAGGAGAGATCTCCCAACATTGGCT	475 bp	DNA	linear	GSS 01-OCT-2003
Qy	23	glnqlypProPvtalProqlYAspProTtrpProqlYalAProProleuPheqluAspPro	471.50			
Db	100	CTGGAGACCCCAATCTCCGTGATCTCCCGGCTGGGGGCGCTCTCTTTTGATGAACT	80.37%			
Qy	43	ProProthArqgProSerArqProTtrpArqAspLeuProqlYuthGlValTtrpProPro	69.16%			
Db	160	CCGGCTCCAGGCTCCACACCGTCTCCGTGAGAGATCTTCTGACAGTGTGCTGGCCCCCA	68.14%			
Qy	63	gluProProArqYtrhArpProProqlAProProArqAspAspProTtrpProqlAqlY				
Db	220	AAGCCCCCAACACATGATCTCCCTTAACCTCTCGCTGATGACCCCTGGCCAGACAGA				
Qy	83	ProqlnProProqlYAspProTtrpProProqlAProqlYAlAspAspArqProqlnlu				
Db	280	ACCAGCCCCCAGAAACCCCTGGCTCTCTGCCCCCTGAGATGACATGAAATCTCAGAG				
Qy	103	gluProAspLeuAspProProArqgluqlYtrArq				
Db	340	GAGCCAGACCTTGACCAACCCAGAGAAAGATATGA				
RESULT 10						
LOCUS	CG473878		475 bp	DNA	linear	GSS 01-OCT-2003
DEFINITION	OS11668 Mus musculus 129Sv/Ev Mus musculus genomic clone OS11668,					
ACCESSION	CG473878					
VERSION	CG473878.1					
KEYWORDS	GSS.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 475)					
AUTHORS	Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richier, L.J., Piggott, U., BeltrandelRio, H., Buxton, E.C., Edwards, U., Finch, R.A., Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaiing, C., Key, B.W., Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Spekreijjs, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, O., Person, C. and Sands, A.T.					
TITLE	Wnt1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention					
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)					
COMMENT	Contact: Zambrowicz BP OmitBank Lexicon Genetics Incorporated 4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: materials@lexgen.com Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11) Class: Gene Trap.					
FEATURES	Location/Qualifiers					
source	1..475 /organism="Mus musculus" /mol_type="genomic DNA" /strain="129Sv/Ev" /db_xref="taxon:10090" /clone="OS11668" /cell_type="embryonic stem cell" /clone_1ib="Mus musculus 129Sv/Ev"					
ORIGIN						
Alignment Scores:						
Prod. NO.:	1.16e-19	Length:	475			
Score:	471.50	Matches:	74			
Percent Similarity:	80.37%	Conservative:	12			
Best Local Similarity:	69.16%	Mismatches:	16			
Query Match:	68.14%	Indels:	5			
DB:	9	Gaps:	1			

US-09-994-365-3 (1-114)	x	CG473878 (1-475)
Qy	7	HisProProAlaGluAspArgGluGluAlaGlySerProThrLeuProGlnGlyProPro 26
Db	40	CACCCA-----CGAAGAGAGATCCCAACCATGCTCTGTGGAGACCCCA 84
Qy	27	ValProGlyAspProTrpProGlyValAlaProLeuPheGluAspProProProThrArg 46
Db	85	ATCCCTGTGTATCCCTGGCTGGGGGGCTCTCTTGTGTATGATGACCTCGCTCCAGGC 144
Qy	47	ProSerArgProTrpArgAspLeuProGluThrArgValTrpProProGluProProArg 66
Db	145	TCCAAACCTCCCTGGAGAGATCTTCTCAAGTGTGTGCTGCTGGCCCCCAACCCCAAGC 204
Qy	67	ThrAspProProGlnProProArgProAspAspProTrpProAlaGlyProGlnProPro 86
Db	205	ACTGATCCCTTAAACCTCTCTGCTGATGACCTCTGGCAGCAGAAACCAAGCCCCCA 264
Qy	87	GluAsnProTrpProProAlaProGluValAlaPheAsnArgProGlnGluGluProAspLeu 106
Db	265	NAAAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 324
Qy	107	AspProProArgGluGluTyr 113
Db	325	GACCCACCCCAAGAAANTAT 345
RESULT 11		
LOCUS	CG474695	322 bp DNA linear GSS 01-OCT-2003
DEFINITION	OSR2738 Mus musculus 129Sv/Ev Mus musculus genomic clone OSR2738,	
ACCESSION	CG474695	
VERSION	CG474695.1	GI:37225584
KEYWORDS	GSS.	
SOURCE	Mus musculus	
ORGANISM	Mus musculus (house mouse)	
REFERENCE	Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 322)	
AUTHORS	Zambrowicz, B. P., Abuln, A., Ramirez-Solis, R., Richter, J. J., Piggott, J., BeltrandelRio, H., Buxton, E. C., Edwards, J., Finch, R. A., Friddle, C. J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jais, C., Key, B. W., Jr., Kipp, P., Konhaufl, B., Ma, Z.-Q., Matkeich, D., Payne, R., Potter, D. G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M. J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sande, A. T.	
TITLE	Mn1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)	
COMMENT	Contact: Zambrowicz BP OmniBank Lexicon Genetics Incorporated 4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: materials@lexgen.com Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11) Class: Gene Trap.	
FEATURES	Location/Qualifiers	
Source	1..322 /organism="Mus musculus" /mol_type="genomic DNA" /strain="129Sv/Ev" /db_xref="taxon:10090" /clone="OSR2738" /cell_type="embryonic stem cell" /clone_11b="Mus musculus 129Sv/Ev"	
ORIGIN		
Alignment Scores:		
Pred. No.:	3,896-19	Length: 322
Score:	460.00	Matches: 74
Percent Similarity:	82.35%	Conservative: 10
Best Local Similarity:	72.55%	Mismatches: 17

```

Query Match: 66.47%   Indels: 1
DB: 9   Gaps: 0

US-09-994-365-3 (1-114) x CG474695 (1-322)

OY 14 G1UG1Ua1aG1ySePProThrLeuProG1nG1yProProValProG1yAspProTriPro 33
   ||| |||
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 AAAAGAGAGAGACTCCCAACATTGCTCTGGAGACCCCAATTCCTGGATGANTCCCTGGGCT 65
   ||| |||

OY 34 G1y1a1aProPoleuPheG1uAspProProProThra1rProSerArGProTriPArGAsp 53
   ||| |||
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 66 GGGGCGCGCTCTTGTGTGATGAACCTCCGCTCCAGGCTCAACCGTCCCTGGAGAGAT 125
   ||| |||
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY 54 LeuProG1uThrG1yVal1TTPProProG1uProProArGThrAspProProG1nProPro 73
   ||| |||
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 126 CTTCTTACACMTGTGTGCTGGCTGGCCCCCAAGCCCCCAAGACCTGATTCCTCAAACTCTCT 185
   ||| |||
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY 74 ArGProAspAspProTriPProAlaG1yProG1nProProG1uAsnProTriPProProAla 93
   ||| |||
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 186 CTGCTTATATGACCCCTTGCCAGACGAGAACCCAGCCCCCAAAAACCCCTGGCTCTGCC 245
   ||| |||
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY 94 ProG1uVala1aPAsnArGProG1nG1uG1uProAspLeuAspPro-ProArG1nG1uTyr 113
   ||| |||
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 246 CCTGAGATGAGCCMTGANTCTCAGAGAGAGCCANAACTTGACCCACCCAGGAGAAAGTA 305
   ||| |||
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY 113 TArG 114
   ||| |||
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 306 TAGA 309

RESULT 12
LOCUS AA763309 332 bp mRNA linear EST 27-JAN-1998
DEFINITION v969ph03.r1 StrataGene mouse skin (#937313) Mus musculus cDNA clone
IMAGE:1229621 5', mRNA sequence.
AA763309
AA763309.1 GI:2813056
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 332)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellander,K., Stepien,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMHI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMHI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watsn.wustl.edu
This clone is available royalty-free through LANT ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:655213
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 329.
Location/Qualifiers
1..332
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1229621"
/sex="female"
/tissue_type="whole skin"
/day_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_id="StrataGene mouse skin (#937313)"

```


THIS PAGE BLANK (USPTO)